

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: February 16, 2005, 08:21:09 ; Search time 496 Seconds  
(without alignments)  
256.679 Million cell updates/sec

Title: US-10-822-254-6  
Perfect score: 554  
Sequence: 1 SQIPASEQETLVKPKLLK.....NLVVNQESSDGTSTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Pending Patents AA Main:*
1:	/cgn2_6/ptodata/1/paa/PCTUS COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US06 COMB.pep.*
3:	/cgn2_6/ptodata/1/paa/US07 COMB.pep.*
4:	/cgn2_6/ptodata/1/paa/US08 COMB.pep.*
5:	/cgn2_6/ptodata/1/paa/US081 COMB.pep.*
6:	/cgn2_6/ptodata/1/paa/US082 COMB.pep.*
7:	/cgn2_6/ptodata/1/paa/US083 COMB.pep.*
8:	/cgn2_6/ptodata/1/paa/US084 COMB.pep.*
9:	/cgn2_6/ptodata/1/paa/US085 COMB.pep.*
10:	/cgn2_6/ptodata/1/paa/US086 COMB.pep.*
11:	/cgn2_6/ptodata/1/paa/US087 COMB.pep.*
12:	/cgn2_6/ptodata/1/paa/US088 COMB.pep.*
13:	/cgn2_6/ptodata/1/paa/US089 COMB.pep.*
14:	/cgn2_6/ptodata/1/paa/US090 COMB.pep.*
15:	/cgn2_6/ptodata/1/paa/US091 COMB.pep.*
16:	/cgn2_6/ptodata/1/paa/US092 COMB.pep.*
17:	/cgn2_6/ptodata/1/paa/US093 COMB.pep.*
18:	/cgn2_6/ptodata/1/paa/US094 COMB.pep.*
19:	/cgn2_6/ptodata/1/paa/US095 COMB.pep.*
20:	/cgn2_6/ptodata/1/paa/US096 COMB.pep.*
21:	/cgn2_6/ptodata/1/paa/US097A COMB.pep.*
22:	/cgn2_6/ptodata/1/paa/US097B COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/US098 COMB.pep.*
24:	/cgn2_6/ptodata/1/paa/US099A COMB.pep.*
25:	/cgn2_6/ptodata/1/paa/US099B COMB.pep.*
26:	/cgn2_6/ptodata/1/paa/US100 COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US101 COMB.pep.*
28:	/cgn2_6/ptodata/1/paa/US102 COMB.pep.*
29:	/cgn2_6/ptodata/1/paa/US103 COMB.pep.*
30:	/cgn2_6/ptodata/1/paa/US104 COMB.pep.*
31:	/cgn2_6/ptodata/1/paa/US105 COMB.pep.*
32:	/cgn2_6/ptodata/1/paa/US106 COMB.pep.*
33:	/cgn2_6/ptodata/1/paa/US107 COMB.pep.*
34:	/cgn2_6/ptodata/1/paa/US108 COMB.pep.*
35:	/cgn2_6/ptodata/1/paa/US109 COMB.pep.*
36:	/cgn2_6/ptodata/1/paa/US110 COMB.pep.*
37:	/cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1  
US-10-822-254-6  
; Sequence 6, Application US/10822254  
; GENERAL INFORMATION:  
; APPLICANT: Taremi, S S  
; APPLICANT: Xie, Gaolian  
; APPLICANT: Hesson, Thomas E  
; APPLICANT: Duca, Jose S  
; APPLICANT: Strickland, Corey  
; APPLICANT: Windsor, William  
; APPLICANT: Madison, Vincent  
; APPLICANT: Zhang, Rumin  
; APPLICANT: Reichert, Paul  
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods  
; FILE REFERENCE: US/10/822,254  
; CURRENT APPLICATION NUMBER: US/10/822,254  
; CURRENT FILING DATE: 2004-04-09  
; PRIOR APPLICATION NUMBER: US 60/461,787

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	554	100.0	109	34	US-10-822-254-6 Sequence 6, Appli
2	551	99.5	109	34	US-10-822-254-10 Sequence 10, Appli
3	548	98.9	109	22	US-09-791-537-88970 Sequence 2, Appli
4	548	98.9	109	34	US-10-822-254-2 Sequence 2, Appli
5	548	98.9	138	21	US-09-724-676-50031 Sequence 50031, A
6	548	98.9	138	21	US-09-724-676-50032 Sequence 50032, A
7	548	98.9	138	21	US-09-724-676A-50031 Sequence 50031, A
8	548	98.9	138	21	US-09-724-676A-50032 Sequence 50032, A
9	548	98.9	209	21	US-09-724-676-50030 Sequence 50030, A
10	548	98.9	209	21	US-09-724-676A-50030 Sequence 50030, A
11	548	98.9	253	35	US-10-990-328-10898 Sequence 10898, A
12	548	98.9	253	37	US-60-505-218-571 Sequence 571, App
13	548	98.9	491	1	PCT-US01-19988-1 Sequence 1, Appli
14	548	98.9	491	1	PCT-US02-29780-8 Sequence 8, Appli
15	548	98.9	491	1	PCT-US03-12946-2602 Sequence 2602, Ap
16	548	98.9	491	1	PCT-US03-34636-22 Sequence 22, Appli
17	548	98.9	491	1	PCT-US04-38193-2236 Sequence 2236, Ap
18	548	98.9	491	1	PCT-US04-12347-1 Sequence 1, Appli
19	548	98.9	491	7	US-08-390-474-2 Sequence 2, Appli
20	548	98.9	491	7	US-08-390-516-2 Sequence 2, Appli
21	548	98.9	491	7	US-08-390-516B-3 Sequence 3, Appli
22	548	98.9	491	7	US-08-390-517-2 Sequence 2, Appli
23	548	98.9	491	7	US-08-390-789-2 Sequence 2, Appli
24	548	98.9	491	14	US-09-029-327-2 Sequence 2, Appli
25	548	98.9	491	19	US-09-587-473-15 Sequence 15, Appli
26	548	98.9	491	22	US-09-791-537-258 Sequence 258, App
27	548	98.9	491	23	US-09-888-077-1 Sequence 1, Appli
28	548	98.9	491	24	US-09-936-035-4 Sequence 4, Appli
29	548	98.9	491	25	US-09-956-425-8 Sequence 8, Appli
30	548	98.9	491	25	US-09-966-724-2 Sequence 2, Appli
31	548	98.9	491	25	US-09-966-724A-2 Sequence 2, Appli
32	548	98.9	491	25	US-09-966-724B-3 Sequence 3, Appli
33	548	98.9	491	28	US-10-219-051B-7482 Sequence 7482, Ap
34	548	98.9	491	28	US-10-228-218A-18 Sequence 18, Appli
35	548	98.9	491	28	US-10-232-951-35 Sequence 35, Appli
36	548	98.9	491	30	US-10-422-536-137 Sequence 137, App
37	548	98.9	491	30	US-10-422-807-28 Sequence 28, Appli
38	548	98.9	491	30	US-10-489-802-8 Sequence 8, Appli
39	548	98.9	491	32	US-10-608-463-2 Sequence 2, Appli
40	548	98.9	491	32	US-10-685-838-1 Sequence 1, Appli
41	548	98.9	491	33	US-10-723-860-2236 Sequence 2236, Ap
42	548	98.9	491	33	US-10-724-225-2 Sequence 2, Appli
43	548	98.9	497	27	US-10-170-205B-31187 Sequence 31187, A
44	548	98.9	497	35	US-10-990-328-10897 Sequence 10897, A
45	548	98.9	497	37	US-60-449-629-132 Sequence 132, App

mine

Rooke  
10/822254 Page 1  
Seq. 10 6 w/ hter

```

; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-254-6

Query Match          100.0%; Score 554; DB 34; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.8e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109

RESULT 2
US-10-822-254-10
; Sequence 10, Application US/108222254
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Duca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-254-10

Query Match          99.5%; Score 551; DB 34; Length 109;
Best Local Similarity 99.1%; Pred. No. 8.9e-59;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109

RESULT 3
US-09-791-537-88970
; Sequence 88970, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
```

```

; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88970
; LENGTH: 109
; TYPE: PRT
; ORGANISM: pdb 1YCRA
US-09-791-537-88970

Query Match          98.9%; Score 548; DB 22; Length 109;
Best Local Similarity 99.1%; Pred. No. 2.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109

RESULT 4
US-10-822-254-2
; Sequence 2, Application US/108222254
; GENERAL INFORMATION:
; APPLICANT: Taremi, S S
; APPLICANT: Xie, Gaolian
; APPLICANT: Hesson, Thomas E
; APPLICANT: Duca, Jose S
; APPLICANT: Strickland, Corey
; APPLICANT: Windsor, William
; APPLICANT: Madison, Vincent
; APPLICANT: Zhang, Rumin
; APPLICANT: Reichert, Paul
; TITLE OF INVENTION: Soluble, Stable Form of Hdm2, Crystalline Forms Thereof and Methods
; FILE REFERENCE: JB06017US01
; CURRENT APPLICATION NUMBER: US/10/822,254
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 60/461,787
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/547,265
; PRIOR FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-254-2

Query Match          98.9%; Score 548; DB 34; Length 109;
Best Local Similarity 99.1%; Pred. No. 2.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 1 SQIPASEQETLVVRPKPLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
Db 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109

RESULT 5
US-09-724-676-50031
; Sequence 50031, Application US/09724676
```

```
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50031
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50031

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 125

RESULT 6
US-09-724-676-50032
; Sequence 50032, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50032
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50032

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 125

RESULT 7
US-09-724-676-50031
; Sequence 50031, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50031
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50031

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 125

RESULT 8
US-09-724-676A-50032
; Sequence 50032, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50032
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-50032

Query Match      98.9%; Score 548; DB 21; Length 138;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 125

RESULT 9
US-09-724-676-50030
; Sequence 50030, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50030
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-50030

Query Match      98.9%; Score 548; DB 21; Length 209;
Best Local Similarity 99.1%; Pred. No. 5.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

Qy 61 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 109
Db 83 CSNDLLGDLFGVPSPFSVKEHRKIYTMIRNLVVNNQESSDSGTSVSEN 131
```

```
RESULT 10
US-09-724-676A-50030
; Sequence 50030, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50030
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-50030

Query Match          98.9%; Score 548; DB 21; Length 209;
Best Local Similarity 99.1%; Pred. No. 5.1e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 131

- RESULT 11
US-10-990-328-10898
; Sequence 10898, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CLO01495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10898
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328-10898

Query Match          98.9%; Score 548; DB 35; Length 253;
Best Local Similarity 99.1%; Pred. No. 6.6e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 131

- RESULT 12
US-60-505-218-571
; Sequence 571, Application US/60505218
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CANCER, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01482
; CURRENT APPLICATION NUMBER: US/60/505,218
; CURRENT FILING DATE: 2003-09-24
```

```
; NUMBER OF SEQ ID NOS: 22507
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-505-218-571

Query Match          98.9%; Score 548; DB 37; Length 253;
Best Local Similarity 99.1%; Pred. No. 6.6e-58;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 23 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 82

QY 61 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 109
Db 83 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 131

- RESULT 13
PCT-US01-19988-1
; Sequence 1, Application PC/TUS0119988
; GENERAL INFORMATION:
; APPLICANT: Ronai, Ze'ev
; TITLE OF INVENTION: Modification of Mdm2 Activity
; FILE REFERENCE: 2420/1H195-US1
; CURRENT APPLICATION NUMBER: PCT/US01/19988
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,343
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19988-1

Query Match          98.9%; Score 548; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSFVKHEHRKIYTMIRNLVVVNNQOESSDGSSTSVSEN 125

- RESULT 14
PCT-US02-29780-8
; Sequence 8, Application PC/TUS0229780
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital, Inc.
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and
; FILE REFERENCE: 44158/243642
; CURRENT APPLICATION NUMBER: PCT/US02/29780
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/956,425
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 491
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29780-8

Query Match      98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPSFSVKEHRKIYTMIRNLVVNNQOESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSFSVKEHRKIYTMIRNLVVNNQOESSDSGTSVSEN 125

RESULT 15
PCT-US03-12946-2602
; Sequence 2602, Application PC/TUS0312946
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000150
; CURRENT APPLICATION NUMBER: PCT/US03/12946
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,827
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2602
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-12946-2602

Query Match      98.9%; Score 548; DB 1; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.6e-57;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPSFSVKEHRKIYTMIRNLVVNNQOESSDSGTSVSEN 109
Db 77 CSNDLLGLDGLFGVPSFSVKEHRKIYTMIRNLVVNNQOESSDSGTSVSEN 125
```

Search completed: February 16, 2005, 08:36:52  
Job time : 498 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:24:14 ; Search time 84 Seconds  
(without alignments)  
51.028 Million cell updates/sec

Title: US-10-822-254-6  
Perfect score: 554  
Sequence: 1 SQIPASEQETLVVRPKPLLLK.....NLVVNQSSDSGTGSVEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 154980 seqs, 39324206 residues

Total number of hits satisfying chosen parameters: 154980

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.\*

- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	311.5	56.2	205	US-10-450-763-60317	Sequence 60317, A
2	246	44.4	140	US-10-499-353A-580	Sequence 580, App
3	246	44.4	148	US-10-499-353A-585	Sequence 585, App
4	246	44.4	343	US-10-499-353A-584	Sequence 584, App
5	225	40.6	107	US-10-499-353A-581	Sequence 581, App
6	184	33.2	361	US-10-450-763-60315	Sequence 60315, A
7	176	31.8	243	US-09-786-702-2	Sequence 2, Appli
8	161	29.1	74	US-10-450-763-60316	Sequence 60316, A
9	75	13.5	254	US-10-450-763-60313	Sequence 60313, A
10	74.5	13.4	236	PCT-1803-06509-5659	Sequence 5659, Ap
11	73.5	13.3	621	US-10-450-763-55457	Sequence 55457, A
12	71	12.8	473	US-10-450-763-5118	Sequence 5118, Ap
13	71	12.8	473	US-60-643-717-15695	Sequence 15695, A
14	70.5	12.7	787	US-10-450-763-55458	Sequence 55458, A
15	69	12.5	291	US-11-031-175-15646	Sequence 15646, A
16	66.5	12.0	422	US-60-643-717-2338	Sequence 2338, Ap
17	66	11.9	2228	US-10-450-763-39401	Sequence 39401, A
18	66	11.9	2275	US-10-489-448-1766	Sequence 1766, Ap
19	64	11.6	488	PCT-US04-20180-30	Sequence 30, Appli
20	64	11.6	971	US-10-450-763-36645	Sequence 36645, A
21	63.5	11.5	498	US-10-450-763-52598	Sequence 52598, A
22	63	11.4	435	US-10-450-763-39688	Sequence 39688, A
23	63	11.4	533	US-10-450-763-39487	Sequence 39487, A
24	62.5	11.3	355	US-60-643-717-12981	Sequence 12981, A
25	62.5	11.3	445	US-10-450-763-45047	Sequence 45047, A

ALIGNMENTS

RESULT 1

US-10-450-763-60317  
; Sequence 60317, Application US/10450763  
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIEP/US

; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11

; PRIOR APPLICATION NUMBER: PCT/US01/08631

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 60317

; LENGTH: 205

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (133)..(194)

; OTHER INFORMATION: p53-associated protein (MDM2) domain identified by Pfam,

; OTHER INFORMATION: accession name MDM2, E-value=7.2e-47, Pfam score of 169.1

US-10-450-763-60317

Query Match 56.2%; Score 311.5; DB 6; Length 205;

Best Local Similarity 73.9%; Pred. No. 2.5e-29;

Matches 68; Conservative 6; Mismatches 9; Indels 9; Gaps 3;

QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTKKEVLVFLGQYIMTKRLYDEKQOHVH 60

|||||

Db 120 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTKKEVLVFLGQYIMTKRLYDEKQOHVH 179

|||||

QY 61 -CSNDLLGDLFGVPSFSVKEHRKIYTMTRYNL 91

|||||

Db 180 DCAN-----LFFPLVDLSIRE---LYISNYITL 203

RESULT 2

US-10-499-353A-580

; Sequence 580, Application US/10499353A

; GENERAL INFORMATION:

; APPLICANT: diadexus, Inc.

; APPLICANT: Sun, Yongming

; APPLICANT: Liu, Chenghua

```
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; PRIOR FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 580
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-580

Query Match          44.4%; Score 246; DB 6; Length 140;
Best Local Similarity 55.4%; Pred. No. 8.3e-22;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAAGEMFTVKEVHMYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMIYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVTL 109

RESULT 3
US-10-499-353A-585
; Sequence 585, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; CURRENT FILING DATE: 2004-06-17
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 585
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-585

Query Match          44.4%; Score 246; DB 6; Length 148;
Best Local Similarity 55.4%; Pred. No. 8.9e-22;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAAGEMFTVKEVHMYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMIYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVTL 109

RESULT 4
US-10-499-353A-584
; Sequence 584, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
```

```
; CURRENT APPLICATION NUMBER: US/10/499,353A
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/342,751
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 584
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-584

Query Match          44.4%; Score 246; DB 6; Length 343;
Best Local Similarity 55.4%; Pred. No. 2.4e-21;
Matches 46; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAAGEMFTVKEVHMYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIYTYMIYRNLVV 94
Db 87 RQSFVKDPSPLYDMLRKNLVTL 109

RESULT 5
US-10-499-353A-581
; Sequence 581, Application US/10499353A
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Endometrial Specific Genes a
; FILE REFERENCE: DEX-0377
; CURRENT APPLICATION NUMBER: US/10/499,353A
; CURRENT FILING DATE: 2004-06-17
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 666
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 581
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-499-353A-581

Query Match          40.6%; Score 225; DB 6; Length 107;
Best Local Similarity 57.5%; Pred. No. 1.8e-19;
Matches 42; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOQHIVHCSNDLLGLDIFG 71
Db 27 VRPKPLLLKLLHAAGAAGEMFTVKEVHMYLGQYIMVKQLYDQEQHVMVYCGDILLGELLG 86

Qy 72 VPSFSVKEHRKIY 84
Db 87 RQSFVKDPSPLY 99

RESULT 6
US-10-450-763-60315
; Sequence 60315, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
```



```
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 60315
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (232)..(261)
; OTHER INFORMATION: Zn-finger in Ran binding protein and others domain identified
; OTHER INFORMATION: by Pfam, accession name zf-RanBP, E-value=3.6e-08, Pfam score of
; OTHER INFORMATION: 40.6
US-10-450-763-60315
```

```
Query Match 33.2%; Score 184; DB 6; Length 361;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVL 38
| | | | | | | | | | | | | | | | | | | | | |
DB 120 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVL 157
```

```
RESULT 7
US-09-786-702-2
; Sequence 2, Application US/09786702
; GENERAL INFORMATION:
; APPLICANT: Luke et al.
; TITLE OF INVENTION: PIPERIZINE-4-PHENYL DERIVATIVES AS INHIBITORS OF THE INTERACTION
; FILE REFERENCE: ASD-FOI-385
; CURRENT APPLICATION NUMBER: US/09/786,702
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 9819860.9
; PRIOR FILING DATE: 1998-09-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-786-702-2
```

```
Query Match 31.8%; Score 176; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE 36
| | | | | | | | | | | | | | | | | | | | |
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKE 52
```

```
RESULT 8
US-10-450-763-60316
; Sequence 60316, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 60316
; LENGTH: 74
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-60316

Query Match 29.1%; Score 161; DB 6; Length 74;
Best Local Similarity 80.9%; Pred. No. 4.1e-12;
Matches 38; Conservative 1; Mismatches 6; Indels 2; Gaps 2;

QY 1 SQIPAS-EQETLVRPKPLLLKLLKSVGAQKDTYTM-KEVLFYLGQYI 45
| | | | | | | | | | | | | | | | | | | | |
DB 21 SQIPSPQETLVRPKPLLLKLLKSVGAQKDTYTYGKRFLENLGQYI 67
```

```
RESULT 9
US-10-450-763-60313
; Sequence 60313, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 60313
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(254)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-60313
```

```
Query Match 13.5%; Score 75; DB 6; Length 254;
Best Local Similarity 29.0%; Pred. No. 0.24;
Matches 40; Conservative 12; Mismatches 34; Indels 52; Gaps 7;

QY 1 SQIPASEQETLVR-----PKPLLL-----KLLKSVGAQKDTYTMKEV----- 37
| | | | | | | | | | | | | | | | | | | | |
DB 120 SQIPASEQETLVRQSESDYQPLLVALFAAKMXKSLKGGKPK-TKKRVNVLVCPLMP 178
| | | | | | | | | | | | | | | | | | | | |

QY 38 -----LFLYQYIMTKRLYDEKQOH-----IVHCSNDLLGLFGVP 73
| | | | | | | | | | | | | | | | | | | | |

DB 179 LNLVXFKVDLKMVALSMKQDILWPAHDAKLLKRNKPCPCVCRQHSND-CANLFLPLV 237
| | | | | | | | | | | | | | | | | | | | |

QY 74 SPSVKEHRKIYTMIRNL 91
| | | | | | | | | | | | | | | | | | | | |

DB 238 DLSIRE---LYISNYITL 252
```

```
RESULT 10
PCT-IB03-06509-5659
; Sequence 5659, Application PC/TIB0306509
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota and The United States of America
; APPLICANT: Secretary of Agriculture
; TITLE OF INVENTION: Mycobacterial Diagnostics
; FILE REFERENCE: 09531/112W01
; CURRENT APPLICATION NUMBER: PCT/IB03/06509
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/137,113
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/362,396
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 5809
; SOFTWARE: FastSeq for Windows Version 4.0
```



```
; OTHER INFORMATION: accession number PR00690A, p-value=9.866e-09, raw score of 10.86
US-10-450-763-55458

Query Match      12.7%; Score 70.5; DB 6; Length 787;
Best Local Similarity 25.5%; Pred. No. 3.1;
Matches 25; Conservative 19; Mismatches 33; Indels 21; Gaps 3;

Qy 1 SQIPASEQ-----ETLVRPKPLLLKLLKSVG---AQKDTYTMKEVLFYLGQYIMTKRLYDE 53
Db 598 STVLASVQGIABEQMENEFPQSAIMQAFQSGFLQPDHILFKQNLFYLETTLNTKOKLYHK 657

Qy 54 K-----QQHIVHCSNDLLGDLFGVPSFSV 77
Db 658 KIFRTAMLFQFVNVLQVLVHKSHDLQBEIGIAYNM 695

RESULT 15
US-11-031-175-15646
; Sequence 15646, Application US/11031175
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/11/031,175
; CURRENT FILING DATE: 2005-01-08
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15646
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(291)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-031-175-15646

Query Match      12.5%; Score 69; DB 7; Length 291;
Best Local Similarity 25.8%; Pred. No. 1.4;
Matches 23; Conservative 23; Mismatches 23; Indels 20; Gaps 6;

Qy 11 LVPRKPLLLKLL---KSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVHCSNDLLG 67
Db 100 LTRYFPPLSPYLHVGRLTGAR-----MKVMAFMGPPYLPEDV-EERTEHVH----LVA 148

Qy 68 DLFGVPFSFVKE---HRKI---YTWIYRN 90
Db 149 GSGAVPNFAILKDALHRLGLKRLHTFLFSN 177

Search completed: February 16, 2005, 08:38:20
Job time : 84 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 166 Seconds  
(without alignments)  
253.957 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASQETIVRPKPLLLK.....NLVVNQESDSGTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	98.9	284	AAR75494	Aar75494 Human dou
2	548	98.9	284	AAR75397	Aar75397 Human dou
3	548	98.9	491	AAR42175	Aar42175 Human MDM
4	548	98.9	491	AAR76696	Aar76696 Human MDM
5	548	98.9	491	AAR76696	Aar76696 Human MDM
6	548	98.9	491	AAR76696	Aar76696 Human MDM
7	548	98.9	491	AAR76696	Aar76696 Human MDM
8	548	98.9	491	AAR76696	Aar76696 Human MDM
9	548	98.9	491	AAR76696	Aar76696 Human MDM
10	548	98.9	491	AAR76696	Aar76696 Human MDM
11	548	98.9	491	AAR76696	Aar76696 Human MDM
12	548	98.9	491	AAR76696	Aar76696 Human MDM
13	548	98.9	491	AAR76696	Aar76696 Human MDM
14	548	98.9	491	AAR76696	Aar76696 Human MDM
15	548	98.9	491	AAR76696	Aar76696 Human MDM
16	548	98.9	491	AAR76696	Aar76696 Human MDM
17	548	98.9	491	AAR76696	Aar76696 Human MDM
18	548	98.9	491	AAR76696	Aar76696 Human MDM
19	548	98.9	491	AAR76696	Aar76696 Human MDM
20	548	98.9	491	AAR76696	Aar76696 Human MDM
21	548	98.9	491	AAR76696	Aar76696 Human MDM
22	548	98.9	491	AAR76696	Aar76696 Human MDM
23	548	98.9	491	AAR76696	Aar76696 Human MDM
24	548	98.9	491	AAR76696	Aar76696 Human MDM
25	548	98.9	491	AAR76696	Aar76696 Human MDM

26	548	98.9	491	8	ADQ19417	Human sof
27	548	98.9	491	8	ADR58893	Human MDM
28	548	98.9	1171	4	AAU32421	Novel hum
29	531.5	95.9	216	3	AAB08846	A human M
30	522.5	94.3	522	7	ADJ95152	Novel NOV
31	522.5	94.3	522	7	ADJ95154	Novel NOV
32	488.5	88.2	489	2	AAR42176	Murine MD
33	488.5	88.2	489	2	AAR76697	Mouse MDM
34	488.5	88.2	489	2	AAW07888	Murine MD
35	488.5	88.2	489	2	AAW15464	Murine MD
36	488.5	88.2	489	2	AAW48242	Mouse MDM
37	488.5	88.2	489	2	AAW57246	Mouse MDM
38	488.5	88.2	489	2	AAW42997	Amino aci
39	488.5	88.2	489	2	AAW42972	Amino aci
40	488.5	88.2	489	2	AAW94305	Mouse MDM
41	488.5	88.2	489	5	AAE25914	Mouse dou
42	488.5	88.2	489	5	ABB57099	Mouse lsc
43	488.5	88.2	489	5	AAO15375	Mouse Dm2
44	488.5	88.2	489	7	ADD21816	Mouse mdm
45	488.5	88.2	489	7	AD661560	Rat Prote

ALIGNMENTS

RESULT 1  
AAR75494  
ID AAR75494 standard; protein; 284 AA.  
XX  
AC AAR75494;  
XX  
XX  
DT 02-FEB-1996 (first entry)  
XX  
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX  
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis; immunoassay.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..284  
FT /note= "amino acids 1-284 of hdm-2 gene product"  
XX  
FN DE4339533-A1.  
XX  
PD 14-JUN-1995.  
XX  
PF 19-NOV-1993; 93DE-04339533.  
XX  
PR 19-NOV-1993; 93DE-04339533.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Zentgraf H, Klein R, Frey M, Martens R;  
XX  
DR WPI; 1995-216248/29.  
XX  
DR N-PSDB; AAQ92515.  
XX  
PT Detection of human double minute gene 2 (hdm-2) antibodies - by  
PT incubation with new hdm-2 or antibody-binding hdm-2 fragments; useful in  
PT the detection of specific cancers.  
XX  
PS Claim 11; Fig 1; 12pp; German.  
XX  
CC Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
CC double minute 2) gene product are claimed. The overlapping protein  
CC fragments contain binding regions for hdm-2- specific antibodies and are  
CC useful for identifying such antibodies in a claimed immunoassay method.  
CC The presence of anti-hdm-2 antibodies is diagnostic of certain forms of  
XX cancer, e.g. rhabdomyosarcoma  
SQ Sequence 284 AA;

Query Match 98.9%; Score 548; DB 2; Length 284;  
Best Local Similarity 99.1%; Pred. No. 3.2e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVH 60  
.. |||||  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVY 76  
|||

QY 61 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125  
|||

RESULT 2  
AAR75397  
ID AAR75397 standard; protein; 284 AA.  
XX  
AC AAR75397;  
XX  
DT 25-MAR-2003 (revised)  
DT 25-JAN-1996 (first entry)  
XX  
DE Human double minute 2 (hdm-2) antibody-binding region fragment 1.  
XX  
KW Human double minute gene 2; hdm-2; antibody binding region; antigen;  
KW cancer; sarcoma; rhabdomyosarcoma; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..284  
FT /note= "amino acids 1-284 of hdm-2 gene product"  
XX  
XX DE4345249-A1.  
XX PD 24-MAY-1995.  
XX  
PF 19-NOV-1993; 93DE-04345249.  
XX  
PR 19-NOV-1993; 93DE-04339533.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Zentgraf H, Klein R, Frey M, Martens R;  
XX  
XX WPI: 1995-195167/26.  
DR N-PSDB; AAQ87261.  
XX  
XX New hdm-2 fragments contg. antibody binding region - used to detect  
PT specific antibodies for diagnosis of cancers, also new DNA sequences  
PT encoding them.  
XX  
XX Claim 2; Fig 1; 11pp; German.  
XX  
XX Fragments contg. amino acids 1-284, 58-284 and 58-491 of the hdm-2 (human  
CC double minute 2) gene product are claimed. The overlapping protein  
CC fragments contain binding regions for hdm-2- specific antibodies and are  
CC useful for identifying such antibodies. The presence of anti-hdm-2  
CC antibodies is diagnostic of certain forms of cancer, e.g.  
CC rhabdomyosarcoma. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 284 AA;

Query Match 98.9%; Score 548; DB 2; Length 284;  
Best Local Similarity 99.1%; Pred. No. 3.2e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVH 60  
.. |||||  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVY 76  
|||

QY 61 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125  
|||

Db 77 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125  
|||

RESULT 3  
AAR42175  
ID AAR42175 standard; protein; 491 AA.  
XX  
AC AAR42175;  
XX  
DT 25-MAR-2003 (revised)  
DT 05-MAY-1994 (first entry)  
XX  
DE Human MDM2.  
XX  
KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;  
KW cellular transformation; carcinoma; human; tumour; MDM2; inhibition;  
KW gene amplification.  
XX  
OS Homo sapiens.  
XX  
PN WO9320238-A2.  
XX  
PD 14-OCT-1993.  
XX  
PF 07-APR-1993; 93WO-US003199.  
XX  
PR 07-APR-1992; 92US-00867840.  
PR 23-JUN-1992; 92US-00903103.  
XX  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;  
XX  
XX WPI: 1993-336944/42.  
DR N-PSDB; AAQ49891.  
XX  
XX Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene  
PT expression, also new DNA, MDM2 protein, antibodies and treatment of  
PT sarcoma by inhibiting MDM2 expression.  
XX  
XX Claim 19; Fig 1; 75pp; English.  
XX  
XX This sequence is encoded by the MDM2 gene. Amplification of the MDM2 gene  
CC is diagnostic of neoplasia or the potential for neoplasia. The protein  
CC encoded by this gene interacts with the product of the p53 gene. p53 is a  
CC tumour suppressor gene and encodes a protein which appears to be a member  
CC of a group of proteins which regulate normal cellular proliferation and  
CC suppression of cellular transformation. Inactivation of the p53 gene has  
CC been implicated in the formation, or progression of a wide variety of  
CC carcinoma. Polypeptides containing at least amino acids 13-41 of p53, or  
CC the DNA encoding these, may be used to inhibit the growth of tumour cells  
CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;  
Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVH 60  
.. |||||  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVY 76  
|||

QY 61 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFVKHRKIYTMIRNLVVNQESSDSGTSVSEN 125  
|||

RESULT 4  
AAR76696  
ID AAR76696 standard; protein; 491 AA.

```

XX AAR76696;
XX 16-OCT-2003 (revised)
XX 01-NOV-1995 (first entry)
XX Human MDM2 protein.
XX MDM2; sarcoma; diagnostic; DNA probe.
XX Homo sapiens; (cell line CaCo-2).
XX US5420263-A.
XX 30-MAY-1995.
XX 07-APR-1993; 93US-00044619.
XX 07-APR-1992; 92US-00867840.
XX 23-JUN-1992; 92US-00903103.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1995-206312/27.
XX N-PSDB; AAQ94589.
XX New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
XX treatment of tumours.
XX Claim 1; Col 23-26; 34pp; English.
XX The human MDM2 gene is genetically altered (i.e. amplified) in human
XX tumour cells. The human MDM2 protein binds to human p53 and allows the
XX cell to escape from p53-regulated growth. Detecting that the gene has
XX become amplified or detecting increased gene product expression (using
XX probes, proteins, antibodies and inhibitors) allows diagnosis and therapy
XX of cancers such as colorectal carcinoma, lung cancer and chronic
XX myelogenous leukaemia. (Updated on 16-OCT-2003 to standardise OS field)
XX PS Sequence 491 AA;
XX
XX Query Match 98.9%; Score 548; DB 2; Length 491;
XX Best Local Similarity 99.1%; Pred. No. 7e-64;
XX Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
XX 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
XX
XX 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNNQESSDGSSTSVSEN 109
XX 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNNQESSDGSSTSVSEN 125
XX
XX RESULT 5
XX AAW07887
XX ID AAW07887 standard; protein; 491 AA.
XX AC AAW07887;
XX 25-MAR-2003 (revised)
XX 28-JAN-1997 (first entry)
XX Human MDM-2, involved in tumour-development.
XX p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
XX antibody fusion protein; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers

```

```

FT Modified-site 166..169
FT /label= phosphorylation site
FT /note= "potential casein kinase II phosphorylation site"
FT Binding-site 181..185
FT /label= nuclear_localisation_signal
FT Modified-site 192..195
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 223..274
FT /label= acid_activation_domain
FT Modified-site 269..272
FT /label= phosphorylation_site
FT /note= "potential casein kinase II phosphorylation site"
FT Modified-site 290..293
FT /label= phosphorylation site
FT /note= "potential casein kinase II phosphorylation site"
FT Domain 305..322
FT /label= metal_binding_site
FT Domain 461..478
FT /label= metal_binding_site
XX US5550023-A.
XX 27-AUG-1996.
XX 18-MAY-1994; 94US-00245500.
XX 07-APR-1992; 92US-00867840.
XX 23-JUN-1992; 92US-00903103.
XX 07-APR-1993; 93US-00044619.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1996-401591/40.
XX N-PSDB; AAT45151.
XX Identification of cpds. interfering with human MDM2/p53 binding - useful
XX as therapeutic agents to treat human neoplastic cells.
XX Claim 26; Col 25-28; 36pp; English.
XX AAW07887 represents human MDM-2 derived from a human colon carcinoma cell
XX line, CaCo-2, cDNA library. The MDM-2 protein is used in a method for
XX identifying compounds that interfere with the binding of p53 and MDM-2.
XX In binding the p53 protein, the MDM-2 protein releases a cell from p53-
XX regulated growth, allowing cancers to develop. Therefore compounds
XX identified as interfering with the binding of MDM-2 to p53 are
XX potentially useful in the treatment of human neoplastic cells. In the
XX method pref. one or both of the proteins is a fusion protein esp. with an
XX antibody or antibody fragment which aids separation and identification.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 491 AA;
XX
XX Query Match 98.9%; Score 548; DB 2; Length 491;
XX Best Local Similarity 99.1%; Pred. No. 7e-64;
XX Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
XX 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
XX
XX 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNNQESSDGSSTSVSEN 109
XX 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNNQESSDGSSTSVSEN 125
XX
XX RESULT 6
XX AAW15463
XX ID AAW15463 standard; protein; 491 AA.
XX

```

```

AC AAW15463;
XX
XX 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
XX Human MDM2.
DE
XX Human; MDM2 protein; antibody; detection; cancer; diagnosis;
XX p53-regulated growth.
XX
XX Homo sapiens.
OS
XX
XX US5618921-A.
FN
XX
XX 08-APR-1997.
PD
XX
XX 17-FEB-1995; 95US-00390479.
PF
XX
XX 07-APR-1992; 92US-00867840.
PR
XX 23-JUN-1992; 92US-00903103.
PR
XX 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Vogelstein B, Kinzler KW, Burrell M, Hill DE;
PI
XX
XX WPI; 1997-225474/20.
DR
XX N-PSDB; AAT66410.
DR
XX
XX Antibodies specific for human MDM2 protein - for diagnosis of cancer.
PT
XX
XX Claim 1; Col 19-24; 35pp; English.
PS
XX
XX This sequence represents the human MDM2 protein. Antibodies that
CC specifically bind to human MDM2 protein may be used for detecting
CC elevated expression of the MDM2 gene in a human tissue or body fluid
CC sample, esp. for cancer diagnosis. The antibodies may be used to
CC interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
CC to sequester p53 and allow the cell to escape from p53-regulated growth.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125
RESULT 7
AAW13380
ID AAW13380 standard; protein; 491 AA.
XX
XX AAW13380;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1997 (first entry)
XX
XX Human MDM2 protein.
DE
XX
XX Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; amplification;
XX elevation; expression; diagnosis; neoplasia; neoplastic transformation;
XX sarcoma; colorectal; lung cancer; chronic myelogenous leukaemia.
XX
XX Homo sapiens.
OS
XX

```

```

FN US5606044-A.
XX
XX 25-FEB-1997.
PD
XX
XX 17-FEB-1995; 95US-00390546.
PF
XX
XX 07-APR-1992; 92US-00867840.
PR
XX 23-JUN-1992; 92US-00903103.
PR
XX 07-APR-1993; 93US-00044619.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Kinzler KW, Vogelstein B, Hill DE, Burrell M;
PI
XX
XX WPI; 1997-153623/14.
DR
XX N-PSDB; AAT62065.
DR
XX
XX Detection of amplification of human MDM2 gene - useful for diagnosis of
PT neoplasia or potential neoplastic transformation.
XX
XX Example 1; Col 21-24; 35pp; English.
PS
XX
XX The present sequence is the human MDM2 protein, the cDNA for which was
CC isolated from a human CaCo-2 colonic carcinoma cell cDNA library using a
CC murine MDM2 cDNA probe. The MDM2 cDNA can be used as a probe to detect
CC the amplification or elevated expression of a human MDM2 gene, which is
CC diagnostic of neoplasia or the potential for neoplastic transformation,
CC useful for the detection of, e.g. sarcomas, colorectal carcinoma, lung
CC cancer and chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 491 AA;
SQ
Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 7e-64;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125
RESULT 8
AAW13600
ID AAW13600 standard; protein; 491 AA.
XX
XX AAW13600;
AC
XX
XX 16-JAN-1998 (first entry)
DT
XX
XX Murine double minute 2 protein sequence.
DE
XX
XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX restenosis.
XX
XX Mus musculus.
OS
XX
XX WO9709343-A2.
FN
XX
XX 13-MAR-1997.
PD
XX
XX 02-SEP-1996; 96WO-FR001340.
PF
XX
XX 04-SEP-1995; 95FR-00010331.
PR
XX
XX (RHON ) RHONE POULENC RORER SA.
PA

```



PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 XX Toque B, Dubs-Peterszman M, Wasylyk B;  
 XX WPI; 1997-192837/17.  
 XX N-PSDB; AAT61637.  
 DR Treating cancer with antagonist of oncogenic activity of protein Mdm2 -  
 PT or nucleic acid encoding an antagonist, also viral vectors contg. this  
 PT nucleic acid.  
 XX Claim 2; Page 26-30; 43pp; French.  
 PS This is the amino acid sequence of the mouse Mdm2 (murine double minute-  
 CC 2) protein, a 90 kD phosphoprotein which binds and modulates the activity  
 CC of the tumour suppressor protein p53. It has now been shown that the mdm2  
 CC protein itself has oncogenic properties, especially in a p53-null  
 CC background. Mdm2 is observed to unblock cell cycle arrest in G1 caused by  
 CC over-expression of the p107 protein. This is especially done by the  
 CC region covering amino acid 1-134. The invention therefore relates to  
 CC antagonists able to inhibit the oncogenic activity of mdm2. These include  
 CC fragments of the p53 protein, especially amino acids 1-52, 1-41, 6-41, 16  
 CC -25 or 18-23 (AAW13602-6), or fragments of transcription factors e.g.  
 CC TFI1, TBP or TAP250, which bind amino acids 1-134 of mdm2. Other  
 CC inhibitors include compounds which disrupt binding to region 135-491 of  
 CC mdm2, e.g. RB, L5 or the transcription factor E2F. The antagonists are  
 CC used to treat e.g. adenocarcinoma of the colon; cancer of the breast,  
 CC lung or stomach; myeloid leukaemia; B cell lymphoma, or other  
 CC hyperproliferative conditions such as restenosis  
 XX Sequence 491 AA;  
 SQ

Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 9  
 AAW48241  
 ID AAW48241 standard; protein; 491 AA.  
 XX AC AAW48241;  
 XX DT 18-JUN-1998 (first entry)  
 XX DE Human MDM2.  
 XX KW Human; MDM2; tumour; cancer; diagnosis; neoplastic disease;  
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.  
 XX OS Homo sapiens.  
 XX FN US5736338-A.  
 XX PD 07-APR-1998.  
 XX PF 17-FEB-1995; 95US-00390517.  
 XX PR 07-APR-1992; 92US-00867840.  
 XX PR 23-JUN-1992; 92US-00903103.  
 XX PR 07-APR-1993; 93US-00044619.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW, Hill DE, Burrell M;  
 XX WPI; 1998-321574/28.  
 XX N-PSDB; AAV28876.  
 XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.  
 XX Claim 1; Col 23-28; 40pp; English.  
 XX A method has been developed for inhibiting the growth of tumour cells  
 CC containing a human MDM2 gene amplification. The method comprises treating  
 CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
 CC of binding to human MDM2 protein. The present sequence represents human  
 CC MDM2 protein. The present invention describes three preferred  
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

XX WPI; 1998-239206/21.  
 DR N-PSDB; AAV20549.  
 XX Cancer diagnosis - by determination of MDM2 protein.  
 XX Claim 1; Col 25-28; 35pp; English.  
 XX The present sequence represents human MDM2 (hMDM2) which is used in the  
 CC method of the present invention. The present invention describes a method  
 CC for diagnosing a neoplastic disease caused by overexpression of MDM2  
 CC protein. The method comprises detecting an elevated cellular amount of  
 CC this protein. The method is useful for the diagnosis of sarcoma,  
 CC especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma  
 XX Sequence 491 AA;  
 SQ

Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 125

RESULT 10  
 AAW57241  
 ID AAW57241 standard; protein; 491 AA.  
 XX AC AAW57241;  
 XX DT 10-AUG-1998 (first entry)  
 XX DE Human MDM2 protein.  
 XX KW Human; p53; MDM2; tumour; growth inhibition; amplification;  
 KW malignant fibrous histiocytoma; liposarcoma.  
 XX OS Homo sapiens.  
 XX FN US5756455-A.  
 XX PD 26-MAY-1998.  
 XX PF 17-FEB-1995; 95US-00390515.  
 XX PR 07-APR-1992; 92US-00867840.  
 XX PR 23-JUN-1992; 92US-00903103.  
 XX PR 07-APR-1993; 93US-00044619.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW;  
 XX WPI; 1998-321574/28.  
 XX N-PSDB; AAV28876.  
 XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
 PT p53 protein fragment.  
 XX Claim 1; Col 23-28; 40pp; English.  
 XX A method has been developed for inhibiting the growth of tumour cells  
 CC containing a human MDM2 gene amplification. The method comprises treating  
 CC the tumour cells with a DNA molecule that expresses a polypeptide capable  
 CC of binding to human MDM2 protein. The present sequence represents human  
 CC MDM2 protein. The present invention describes three preferred  
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises amino

CC acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises amino  
 CC acids 13-41 of p53 (see AAW57240) and at least none additional p53  
 CC residues on the N- or C-terminal side, provided that the polypeptide  
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide  
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine  
 CC additional p53 residues on the N- or C-terminal side, provided that the  
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous  
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so  
 CC detection of increased expression of MDM2 gene products indicates  
 CC tumourigenesis  
 XX Sequence 491 AA;  
 SQ Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 76  
 Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125  
 RESULT 11  
 AAW42879  
 ID AAW42879 standard; protein; 491 AA.  
 XX AC AAW42879;  
 XX DT 30-APR-1998 (first entry)  
 DE Amino acid sequence of human MDM2.  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX OS Homo sapiens.  
 XX PN US5708136-A.  
 XX PD 13-JAN-1998.  
 XX PF 17-FEB-1995; 95US-00390516.  
 XX PR 07-APR-1992; 92US-00867840.  
 XX PR 23-JUN-1992; 92US-00903103.  
 XX PR 07-APR-1993; 93US-00044619.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW, Burrell M, Hill DE;  
 XX WPI; 1998-100408/09.  
 XX Human MDM2 binding polypeptide - comprises fragments of p53, useful in re  
 XX -establishing p53-regulated growth control in cells over-expressing MDM2.  
 XX Disclosure; Col 23-28; 41pp; English.  
 XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-

CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour  
 CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
 CC escape from p53-regulated growth, compounds that inhibit such binding  
 CC would be useful as anti-cancer agents  
 XX Sequence 491 AA;  
 SQ Query Match 98.9%; Score 548; DB 2; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 76  
 Qy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125  
 RESULT 12  
 AAW42971  
 ID AAW42971 standard; protein; 491 AA.  
 XX AC AAW42971;  
 XX DT 29-APR-1998 (first entry)  
 DE Amino acid sequence of human MDM2.  
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein; p53 polypeptide;  
 KW binding; tumour cell; p53-regulated growth; inhibition;  
 KW anti-cancer agent.  
 XX OS Homo sapiens.  
 XX PN US702903-A.  
 XX PD 30-DEC-1997.  
 XX PF 13-NOV-1995; 95US-00557393.  
 XX PR 07-APR-1992; 92US-00867840.  
 XX PR 23-JUN-1992; 92US-00903103.  
 XX PR 07-APR-1993; 93US-00044619.  
 XX PR 18-MAY-1994; 94US-00245500.  
 XX PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX PI Vogelstein B, Kinzler KW;  
 XX WPI; 1998-076411/07.  
 XX N-PSDB; AAV03607.  
 XX Cell containing reporter construct containing human MDM2 and p53 genes -  
 XX for identifying compounds that interfere with binding of human MDM2 to  
 XX human p53, useful as anti-cancer agents.  
 XX Disclosure; Coulms 22-28; 37pp; English.  
 XX The present sequence represents human MDM2. The MDM2 gene is amplified in  
 CC some human tumours. The amplification of this gene is diagnostic of  
 CC neoplasia or its potential. It is speculated that the MDM2 protein is a  
 CC potential DNA binding protein that functions in the modulation of  
 CC expression of other genes and, when present in excess, interferes with  
 CC normal constraints on cell growth. A cell containing three recombinant  
 CC DNA constructs was produced. These constructs encode an MDM2 protein  
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused  
 CC to a transcriptional activation domain, and a reporter gene downstream  
 CC from a DNA element which is recognised by the sequence-specific DNA-  
 CC binding domain. The cell is used to identify a compound which interferes  
 CC with the binding of MDM2 and p53. Since MDM2 is overexpressed in tumour

CC cells and since binding of MDM2 to p53 appears to allow tumour cells to  
CC escape from p53-regulated growth, compounds that inhibit such binding  
CC would be useful as anti-cancer agents

SQ Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 7e-64; Indels 0; Gaps 0;  
Matches 108; Conservative 1; Mismatches 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 125

#### RESULT 13

AAW94304  
ID AAW94304 standard; protein; 491 AA.

AC AAW94304;

DT 13-APR-1999 (first entry)

XX Human MDM2.

XX Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;  
KW malignant fibrous histiocytoma; MFH; liposarcoma.

XX Homo sapiens.

XX US858976-A.

XX 12-JAN-1999.

XX 14-FEB-1997; 97US-00801718.

XX 07-APR-1992; 92US-00867840.

XX 23-JUN-1992; 92US-00903103.

XX 07-APR-1993; 93US-00044619.

XX 17-FEB-1995; 95US-00390515.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Kinzler KW, Vogelstein B;

XX WPI; 1999-152105/13.

XX N-PSDB; AAX03947.

XX Inhibiting growth of tumour cells having MDM2 gene amplification - with  
XX MDM2-binding p53 fragment.

XX Claim 1; Col 23-28; 41pp; English.

XX The present invention describes: (1) a method for inhibiting the growth  
XX of tumour cells which contain a human MDM2 gene amplification, comprising  
XX administering to the cells a DNA molecule that expresses a polypeptide  
XX consisting of a portion of p53 i.e. amino acids 13-41 of the 64 amino  
XX acid sequence given in AAW94304, the polypeptide being capable of binding  
XX to human MDM2 (the present sequence); (2) a method as in (1) where the  
XX polypeptide lacks the homo-oligomerisation domain of p53; and (3) a  
XX method as in (1) where the polypeptide lacks amino acids 138-393 of p53.  
XX The method is useful for treating the following tumour types which have a  
XX MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH), M-20  
XX MFH, L-9 liposarcoma, K-7 liposarcoma, K-28 liposarcoma, K-30  
XX liposarcoma, and OSA-CL MFH

SQ Sequence 491 AA;

Query Match 98.9%; Score 548; DB 2; Length 491;

Best Local Similarity 99.1%; Pred. No. 7e-64;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
DB 17 SQIPASEQETLVPRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 109  
DB 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVNQESSDSTSVSEN 125

#### RESULT 14

AAI96567  
ID AAY96567 standard; protein; 491 AA.

AC AAY96567;

DT 12-SEP-2000 (first entry)

XX MDM2 oncoprotein.

XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;  
KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;  
KW proliferation; immortal; tumour therapy; macular degeneration; activator;  
XX INK4; MDM2; oncoprotein.

XX Homo sapiens.

XX WO200031238-A2.

XX 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027907.

XX 25-NOV-1998; 98US-0109891P.

XX 17-FEB-1999; 99US-0120549P.

XX (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;

XX WPI; 2000-400055/34.

XX N-PSDB; AAA29389.

XX New method for increasing the proliferative capacity of cell lines  
XX comprises administering agents reversibly activating telomerase activity  
XX and reversibly inactivating Rb/INK4 and/or p53 pathways useful in  
XX treating age related diseases.

XX Claim 5; Page 120; 123pp; English.

XX The invention concerns methods and reagents for extending the life-span,  
XX e.g. the number of mitotic divisions, of a cell. The method relies on  
XX activation of a telomerase activity and inhibition of one or both of a  
XX retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb  
XX by cyclin-dependent kinases, cdk4 and cdk6, releases the cells into the  
XX division cycle. Binding of INK4 family members, e.g. the tumour  
XX suppressor p16INK4a, inhibits kinase activity and results in growth  
XX arrest. Rb inactivators can selectively and reversibly inactivate an  
XX Rb/INK4 pathway, especially an Rb/p16INK4a pathway. The oncoprotein MDM2  
XX is a cellular inhibitor of Rb/E2F function and the p53 tumour suppressor  
XX and can also be used in the methods. Other molecules which can be used  
XX include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which  
XX differs from at one or more of residues K22, R24, H95 and/or D97.

XX Additional constructs include a papilloma virus E7 protein, or other  
XX viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of  
XX the Rb and p16INK4a genes may also be used. The methods are useful for  
XX increasing the proliferative capacity of cells. The cells are  
XX subsequently of use in pharmaceutical and cosmetic preparations used to  
XX treat conditions related to (premature) ageing, e.g. macular degeneration  
XX and arteriosclerosis. The cells can also be used to replace tumour cell  
XX lines in vitro and for studies on biochemical and physiological aspects

CC of growth and differentiation. Long lived (immortal) cells could also be  
 CC of use in the production of normal or genetically engineered  
 CC biotechnology products  
 XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 3; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
 DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 76

QY 61 CSNDLLGDLFGVPSPSVKHEHRIYTMIRNLLVNVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPSVKHEHRIYTMIRNLLVNVNQESSDSGTSVSEN 125

RESULT 15  
 AAB48284  
 ID AAB48284 standard; protein; 491 AA.

AC AAB48284;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX Human MDM2 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic.

XX Homo sapiens.  
 XX WO2000075184-A1.

PD 14-DEC-2000.  
 XX  
 PF 05-JUN-2000; 2000WO-US015449.  
 XX  
 PR 04-JUN-1999; 99US-0137494P.

XX (UYA ) UNIV YALE.  
 PA  
 XX Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.  
 DR N-PSDB; AAC84596.

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins.

PS Claim 5; Page 93-95; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
 CC cullin/CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours

XX Sequence 491 AA;

Query Match 98.9%; Score 548; DB 4; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 7e-64;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 76  
 QY 61 CSNDLLGDLFGVPSPSVKHEHRIYTMIRNLLVNVNQESSDSGTSVSEN 109  
 DB 77 CSNDLLGDLFGVPSPSVKHEHRIYTMIRNLLVNVNQESSDSGTSVSEN 125

Search completed: February 16, 2005, 08:27:42  
 Job time : 168 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:09 ; Search time 43 Seconds  
(without alignments)  
189.227 Million cell updates/sec

Title: US-10-822-254-6  
Perfect score: 554  
Sequence: 1 SQIPASEQETLVPRKPLLLK.....NLVVNQSSDSTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pap.\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pap.\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pap.\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pap.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS COMB.pap.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	98.9	188	4	US-09-603-052-4
2	548	98.9	491	1	US-07-903-103-2
3	548	98.9	491	1	US-08-044-619A-2
4	548	98.9	491	1	US-08-283-911-2
5	548	98.9	491	1	US-08-245-500A-3
6	548	98.9	491	1	US-08-390-546-3
7	548	98.9	491	1	US-08-390-479A-3
8	548	98.9	491	1	US-08-557-393-3
9	548	98.9	491	1	US-08-390-516C-3
10	548	98.9	491	1	US-08-390-517A-3
11	548	98.9	491	1	US-08-390-515A-3
12	548	98.9	491	2	US-08-801-718-3
13	548	98.9	491	3	US-09-170-159A-3
14	548	98.9	491	4	US-09-480-718-4A
15	548	98.9	528	4	US-09-949-016-7125
16	548	98.9	528	4	US-09-949-016-7126
17	548	98.9	528	4	US-09-949-016-7127
18	548	98.9	528	4	US-09-949-016-7128
19	548	98.9	528	4	US-09-949-016-7129
20	531.5	95.9	216	3	US-09-510-252-4
21	488.5	88.2	489	1	US-07-903-103-4
22	488.5	88.2	489	1	US-08-044-619A-4
23	488.5	88.2	489	1	US-08-283-911-4
24	488.5	88.2	489	1	US-08-245-500A-5
25	488.5	88.2	489	1	US-08-390-546-5
26	488.5	88.2	489	1	US-08-390-479A-5
27	488.5	88.2	489	1	US-08-557-393-5

28	488.5	88.2	489	1	US-08-390-516C-5
29	488.5	88.2	489	1	US-08-390-517A-5
30	488.5	88.2	489	1	US-08-390-515A-5
31	488.5	88.2	489	2	US-08-801-718-5
32	488.5	88.2	489	3	US-09-170-159A-5
33	488.5	88.2	489	4	US-09-480-718-46
34	244	44.0	490	4	US-09-949-016-6218
35	161	29.1	365	4	US-09-949-016-11388
36	71.5	12.9	420	4	US-09-270-767-43304
37	69.5	12.5	244	4	US-09-543-681A-6675
38	69	12.5	291	4	US-09-902-540-15646
39	68	12.3	766	4	US-09-248-796A-16626
40	67	12.1	2938	5	PCT-US94-00198-3
41	65	11.7	62	4	US-09-248-796A-24446
42	65	11.7	384	4	US-08-504-617-2
43	64	11.6	310	4	US-09-408-020-44
44	64	11.6	354	4	US-09-198-452A-317
45	64	11.6	354	4	US-09-438-185A-305

ALIGNMENTS

RESULT 1

US-09-603-052-4  
; Sequence 4, Application US/09603052  
; Patent No. 6492116  
; GENERAL INFORMATION:  
; APPLICANT: Chene, Patrick  
; APPLICANT: Hochkeppel, Heinz-Kurt  
; TITLE OF INVENTION: Assay for identifying inhibitors of the interaction  
; FILE REFERENCE: MEWB26.001C1  
; CURRENT APPLICATION NUMBER: US/09/603,052  
; CURRENT FILING DATE: 2000-06-26  
; PRIOR APPLICATION NUMBER: EP 95810576.9  
; PRIOR FILING DATE: 1995-09-18  
; PRIOR APPLICATION NUMBER: PCT/EP96/03957  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-603-052-4

Query Match	98.9%	Score 548;	DB 4;	Length 188;
Best Local Similarity	99.1%	Pred. No. 5.4e-61;		
Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SOIPASEQETLVPRKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60		
Db	17	SOIPASEQETLVPRKPLLLKLLKSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHVY 76		
QY	61	CSNDLLGDLFGVPSFVKEHRKIYTMVYRNLVVNQSSDSTSVSEN 109		
Db	77	CSNDLLGDLFGVPSFVKEHRKIYTMVYRNLVVNQSSDSTSVSEN 125		

RESULT 2

US-07-903-103-2  
; Sequence 2, Application US/07903103  
; Patent No. 5411860  
; GENERAL INFORMATION:  
; APPLICANT: VOGELSTEIN, BERT  
; APPLICANT: KINZLER, KENNETH  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G ST., N.W.

```
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903,103
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-903-103-2
;
; Query Match 98.9%; Score 548; DB 1; Length 491;
; Best Local Similarity 99.1%; Pred. No. 1.9e-60;
; Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
; DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76
;
; QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
; DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125
;
; US-07-903-103-2
;
; Query Match 98.9%; Score 548; DB 1; Length 491;
; Best Local Similarity 99.1%; Pred. No. 1.9e-60;
; Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60
; DB 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76
;
; QY 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109
; DB 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125
;
; RESULT 3
; US-08-044-619A-2
; Sequence 2, Application US/08044619A
; Patent No. 5420263
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
;
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;
; RESULT 4
; US-08-283-911-2
; Sequence 2, Application US/08283911
; Patent No. 5519118
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,911
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
```

;  
; LENGTH: 491 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-283-911-2

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 125

RESULT 5  
US-08-245-500A-3  
; Sequence 3, Application US/08245500A  
; Patent No. 5550023  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/245.500A  
; FILING DATE: 07-APR-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.42798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX: 197430 BMB UT  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-245-500A-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 125

Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 125

RESULT 6  
US-08-390-546-3  
; Sequence 3, Application US/08390546  
; Patent No. 5606044  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
; STREET: 1001 G STREET, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390.546  
; FILING DATE: 07-APR-1993  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAGAN, SARAH A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.42798  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; TELEX: 197430 BMB UT  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-390-546-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60  
Db 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDGSSTSVSEN 125

RESULT 7  
US-08-390-479A-3  
; Sequence 3, Application US/08390479A  
; Patent No. 5618921  
; GENERAL INFORMATION:  
; APPLICANT: BURRELL, MARILEE  
; APPLICANT: HILL, DAVID E.  
; APPLICANT: KINZLER, KENNETH W.  
; APPLICANT: VOGELSTEIN, BERT  
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
; TITLE OF INVENTION: HUMAN TUMORS  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390.479A  
FILING DATE: 02-FEB-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.48992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-390-479A-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHVH 60  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHVY 76  
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 8  
US-08-557-393-3  
Sequence 3, Application US/08557393  
Patent No. 5702903  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/557,393  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,500  
FILING DATE: 18-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-557-393-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHVH 60  
Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKDTYTMKEVLVYLGQYIMTKRLYDEKQOHVY 76  
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 125

RESULT 9  
US-08-390-516C-3  
Sequence 3, Application US/08390516C  
Patent No. 5708136  
GENERAL INFORMATION:  
APPLICANT: BURRELL, MARILEE  
APPLICANT: HILL, DAVID E.  
APPLICANT: KINZLER, KENNETH W.  
APPLICANT: VOGELSTEIN, BERT  
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
TITLE OF INVENTION: HUMAN TUMORS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
STREET: 1001 G STREET, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,516C  
FILING DATE: 07-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KAGAN, SARAH A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 01107.42798  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-508-9100  
TELEFAX: 202-508-9299  
TELEX: 197430 BMB UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein



US-08-390-516C-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 10

US-08-390-517A-3  
 ; Sequence 3, Application US/08390517A  
 ; Patent No. 5736338  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,517A  
 FILING DATE: 07-APR-1993  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-390-517A-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 11

US-08-390-515A-3

; Sequence 3, Application US/08390515A  
 ; Patent No. 5756455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20001

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/390,515A  
 FILING DATE: 07-APR-1993  
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
 NAME: KAGAN, SARAH A.  
 REGISTRATION NUMBER: 32,141  
 REFERENCE/DOCKET NUMBER: 01107.42798  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-508-9100  
 TELEFAX: 202-508-9299  
 TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-390-515A-3

Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 1.9e-60;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60  
 Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 109  
 Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVNVNQESSDSGTSVSEN 125

RESULT 12

US-08-801-718-3  
 ; Sequence 3, Application US/08801718  
 ; Patent No. 5858976  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BURRELL, MARILEE  
 ; APPLICANT: HILL, DAVID E.  
 ; APPLICANT: KINZLER, KENNETH W.  
 ; APPLICANT: VOGELSTEIN, BERT  
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN  
 ; TITLE OF INVENTION: HUMAN TUMORS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT  
 ; STREET: 1001 G STREET, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.

```
;
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,718
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,515
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BEMB UT
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-718-3

Query Match 98.9%; Score 548; DB 2; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Oy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 14
US-09-480-718-44
; Sequence 44, Application US/09480718
; Patent No. 6407062
; GENERAL INFORMATION:
; APPLICANT: Sheri, Charles J
; APPLICANT: Quelle, Dawn E
; APPLICANT: Weber, Jason D
; APPLICANT: Rousset, Martine F.
; APPLICANT: Frederique, Zindy
; TITLE OF INVENTION: ARF-19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
; FILE REFERENCE: 1340-1-023 CIP 1
; CURRENT APPLICATION NUMBER: US/09/480,718
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 09/129,855
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-480-718-44

Query Match 98.9%; Score 548; DB 4; Length 491;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

Oy 61 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 109
Db 77 CSNDLLGDLFGVPFSVKEHRKIYTMIRNLVVNNQESSDSTSVSEN 125

RESULT 15
US-09-949-016-7125
; Sequence 7125, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7125
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7125

Query Match          98.9%; Score 548; DB 4; Length 528;
Best Local Similarity 99.1%; Pred. No. 2.1e-60;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  SQIPASEQETLVRPKPLLLKLLKSVGAQKDTVTMKEVLFYLGQYIMTKRLYDEKQQHIVH 60
      |||
Db       54  SQIPASEQETLVRPKPLLLKLLKSVGAQKDTVTMKEVLFYLGQYIMTKRLYDEKQQHIVY 113
      |||

QY      61  CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 109
      |||
Db      114  CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVVNQESSDSGTSVSEN 162
      |||
```

Search completed: February 16, 2005, 08:28:30  
Job time : 45 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:24:54 ; Search time 697 Seconds  
(without alignments)  
51.098 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	548	98.9	491	US-09-888-077-1	Sequence 1, Appli
2	548	98.9	491	US-09-956-425-8	Sequence 8, Appli
3	548	98.9	491	US-09-029-327-2	Sequence 2, Appli
4	548	98.9	491	US-09-966-724-2	Sequence 2, Appli
5	548	98.9	491	US-10-422-536-137	Sequence 137, App
6	548	98.9	491	US-10-232-951-35	Sequence 35, Appli
7	548	98.9	491	US-10-685-838-1	Sequence 1, Appli
8	531.5	95.9	216	US-10-057-510-4	Sequence 4, Appli
9	522.5	94.3	522	US-10-287-226-380	Sequence 380, App
10	522.5	94.3	522	US-10-287-226-382	Sequence 382, App
11	488.5	88.2	489	US-09-956-425-6	Sequence 6, Appli
12	488.5	88.2	489	US-09-966-724-4	Sequence 4, Appli
13	481	86.8	95	US-10-685-838-2	Sequence 2, Appli

14	472	85.2	95	16	US-10-685-838-4	Sequence 4, Appli
15	468	84.5	92	16	US-10-685-838-3	Sequence 3, Appli
16	309	55.8	59	14	US-10-211-088-143	Sequence 143, App
17	74.5	13.4	578	16	US-10-437-963-174237	Sequence 174237,
18	73.5	13.3	467	15	US-10-362-774-3	Sequence 3, Appli
19	73.5	13.3	467	15	US-10-369-493-6071	Sequence 6071, Ap
20	73	13.2	613	16	US-10-437-963-113326	Sequence 113326,
21	72	13.0	967	15	US-10-437-963-113326	Sequence 113326,
22	71	12.8	472	15	US-10-369-493-16585	Sequence 16585, A
23	71	12.8	473	15	US-10-282-122A-45311	Sequence 45311, A
24	70.5	12.7	79	15	US-10-424-599-236213	Sequence 236213,
25	70.5	12.7	350	10	US-09-746-783-54	Sequence 54, Appl
26	70.5	12.7	709	15	US-10-282-122A-63455	Sequence 63455, A
27	70.5	12.7	837	16	US-10-408-765A-2452	Sequence 2452, Ap
28	70	12.6	969	15	US-10-335-977-7410	Sequence 7410, Ap
29	70	12.6	972	15	US-10-335-977-7410	Sequence 7410, Ap
30	68	12.3	438	14	US-10-176-584A-2	Sequence 2, Appli
31	67.5	12.2	434	15	US-10-424-599-257589	Sequence 257589,
32	67.5	12.2	438	10	US-09-769-787-48	Sequence 48, Appl
33	67	12.1	368	15	US-10-389-566-382	Sequence 382, App
34	67	12.1	3092	9	US-09-801-368-172	Sequence 172, App
35	67	12.1	3092	15	US-10-369-493-1470	Sequence 1470, Ap
36	66.5	12.0	225	15	US-10-282-122A-52429	Sequence 52429, A
37	66.5	12.0	277	15	US-10-282-122A-75363	Sequence 75363, A
38	66.5	12.0	291	15	US-10-425-114-59572	Sequence 59572, A
39	66.5	12.0	372	16	US-10-437-963-169953	Sequence 169953,
40	66.5	12.0	422	15	US-10-369-493-7027	Sequence 7027, Ap
41	66.5	12.0	816	15	US-10-282-122A-61368	Sequence 61368, A
42	66	11.9	185	15	US-10-389-566-818	Sequence 818, App
43	66	11.9	320	16	US-10-437-963-133574	Sequence 133574,
44	66	11.9	418	15	US-10-389-566-819	Sequence 819, App
45	66	11.9	432	15	US-10-389-566-2420	Sequence 2420, App

ALIGNMENTS

RESULT 1  
US-09-888-077-1  
; Sequence 1, Application US/09888077  
; Patent No. US20020031818A1  
; GENERAL INFORMATION:  
; APPLICANT: Ronai, Ze'ev  
; APPLICANT: Fuchs, Serge  
; TITLE OF INVENTION: Modification of Mdm2 Activity  
; FILE REFERENCE: 2420/1H195-US1  
; CURRENT APPLICATION NUMBER: US/09/888,077  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,343  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 491  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-888-077-1

Query Match	98.9%	Score 548;	DB 9;	Length 491;
Best Local Similarity	99.1%	Pred. No. 2.8e-56;		
Matches 108;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SOIPASEQETLVVRPKPLLLKLLKSVGAQKQTYTWMKEVLFYLGQYIMTKRLYDEKQKHIVH	60	
Db	17	SOIPASEQETLVVRPKPLLLKLLKSVGAQKQTYTWMKEVLFYLGQYIMTKRLYDEKQKHIVY	76	
QY	61	CSNDLLGLFGVPFSVKEHKIYTMIVRNLVVNNQESSDSGTSVSEN	109	
Db	77	CSNDLLGLFGVPFSVKEHKIYTMIVRNLVVNNQESSDSGTSVSEN	125	
RESULT 2				
US-09-956-425-8				

```

; Sequence 8, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-425-8

Query Match      98.9%; Score 548; DB 9; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQSSDSGTSVSEN 125

RESULT 3
US-09-029-327-2
; Sequence 2, Application US/09029337
; Publication No. US20030060432A1
; GENERAL INFORMATION:
; APPLICANT: TOCQUE, Bruno
; APPLICANT: WASIYLYK, Bohdan
; APPLICANT: DUBS-POTERSZMAN,
; APPLICANT: Marie-Christine
; TITLE OF INVENTION: ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF
; TITLE OF INVENTION: THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF
; TITLE OF INVENTION: CANCERS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/029,327
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 96/01340
; FILING DATE: 02-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR95/10331
; FILING DATE: 04-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehlner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95050-US
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808

```

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-029-327-2

Query Match      98.9%; Score 548; DB 10; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60
DB 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQSSDSGTSVSEN 109
DB 77 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLLVNVNQSSDSGTSVSEN 125

RESULT 4
US-09-966-724-2
; Sequence 2, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBME UT
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-724-2

Query Match      98.9%; Score 548; DB 11; Length 491;
Best Local Similarity 99.1%; Pred. No. 2.8e-56;
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Query Match	98.9%	Score 548;	DB 15;	Length 491;
Best Local Similarity	99.1%	Pred. No. 2.8e-56;		
Matches 108; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

Local Similarity 55.1%; Freq. NO: 2.0E-30;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SQIPASEQETLVRPKPLLLKLLKSVAQAQTWTMKEVLFYLGQVIMTKRLYDEKQHIVH	60
Dp	17	SQIPASEQETLVRPKPLLLKLLKSVAQAQTWTMKEVLFYLGQVIMTKRLYDEKQHIVY	76

RESULT 8  
US-10-057-510-4  
Sequence 4, Application US/10057510  
Publication No. US20020098580A1  
GENERAL INFORMATION:  
APPLICANT: Nandabalan, Krishnan  
APPLICANT: Yang, Meljia  
APPLICANT: Schulz, Vincent  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF  
FILE REFERENCE: 15966-524 MDM US  
CURRENT APPLICATION NUMBER: US/10/057,510  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: USSN 09/510,252  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: USSN 60/121,192  
PRIOR FILING DATE: 1999-02-23

; PRIOR APPLICATION NUMBER: USN 60/122,643  
 ; PRIOR FILING DATE: 1999-03-03  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 216  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-057-510-4

Query Match 95.9%; Score 531.5; DB 13; Length 216;  
 Best Local Similarity 98.2%; Pred. No. 8.7e-55;  
 Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKQYITMKELFYLGVYIMTKRLYDEKQOHVH 60

Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKQYITMKELFYLGVYIMTKRLYDEKQOHVY 75

Qy 61 CSNDLLGDLFGVPSPVSKHRKIYTMIRNLVNVNQESSDSGTSVSEN 109

Db 76 CSNDLLGDLFGVPSPVSKHRKIYTMIRNLVNVNQESSDSGTSVSEN 124

# RESULT 9

US-10-287-226-380  
 ; Sequence 380, Application US/10287226  
 ; Publication No. US20040086875A1

## GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,  
 ; APPLICANT: Alsobrook, John P.,  
 ; APPLICANT: Berghs, Constance,  
 ; APPLICANT: Boldog, Ference,  
 ; APPLICANT: Burgess, Catherine E.,  
 ; APPLICANT: Chant, John S.,  
 ; APPLICANT: Chaudhuri, Amitabha,  
 ; APPLICANT: DiPippo, Vincent A.,  
 ; APPLICANT: Edinger, Shlomit R.,  
 ; APPLICANT: Eisen, Andrew,  
 ; APPLICANT: Ellerman, Karen,  
 ; APPLICANT: Gangolli, Esha A.,  
 ; APPLICANT: Gorman, Linda,  
 ; APPLICANT: Gerlach, Valerie,  
 ; APPLICANT: Ji, Weizhen,  
 ; APPLICANT: Kekuda, Ramesh,  
 ; APPLICANT: Khrantsov, Nikolai,  
 ; APPLICANT: Li, Li,  
 ; APPLICANT: Malyankar, Uriel M.,  
 ; APPLICANT: MacDougall, John R.,  
 ; APPLICANT: Mezes, Peter S.,  
 ; APPLICANT: Miller, Charles E.,  
 ; APPLICANT: Millet, Isabelle,  
 ; APPLICANT: Ooi, Chean Eng,  
 ; APPLICANT: Ort, Tatiana,  
 ; APPLICANT: Padigaru, Muralidhara,  
 ; APPLICANT: Pattarajan, Meera,  
 ; APPLICANT: Rastelli, Luca,  
 ; APPLICANT: Rieger, Daniel K.,  
 ; APPLICANT: Rothenberg, Mark E.,  
 ; APPLICANT: Shenoy, Suresh G.,  
 ; APPLICANT: Spaderna, Steven K.,  
 ; APPLICANT: Spytek, Kimberley A.,  
 ; APPLICANT: Taupier, Jr., Raymond J.,  
 ; APPLICANT: Vernet, Corine A.M.,  
 ; APPLICANT: Zerhusen, Bryan D.,  
 ; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-480C

; CURRENT APPLICATION NUMBER: US/10/287,226  
 ; CURRENT FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: 60/334,421  
 ; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,392  
 ; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/360,148  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: 60/364,000  
 ; PRIOR FILING DATE: 2002-03-13  
 ; PRIOR APPLICATION NUMBER: 60/404,821  
 ; PRIOR FILING DATE: 2002-08-20  
 ; PRIOR APPLICATION NUMBER: 60/334,526  
 ; PRIOR FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 60/354,409  
 ; PRIOR FILING DATE: 2002-02-04  
 ; PRIOR APPLICATION NUMBER: 60/364,227  
 ; PRIOR FILING DATE: 2002-03-13  
 ; PRIOR APPLICATION NUMBER: 60/334,027  
 ; PRIOR FILING DATE: 2001-11-28  
 ; PRIOR APPLICATION NUMBER: 60/331,641  
 ; PRIOR FILING DATE: 2001-11-20  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 673  
 ; SOFTWARE: Curasequid version 0.1  
 ; SEQ ID NO 380  
 ; LENGTH: 522  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-287-226-380

Query Match 94.3%; Score 522.5; DB 15; Length 522;  
 Best Local Similarity 77.1%; Pred. No. 3.3e-53;  
 Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

Qy 1 SQIPASEQETLVPRKPLLLKLLKSVGAQKQYITMKELFYLGVYIMTKRLYDEKQOHVH 36

Db 17 SQIPASEQETLVPRKPLLLKLLKSVGAQKQYITMKELFYLGVYIMTKRLYDEKQOHVH 76

Qy 37 -----VLFYLGQYIMTKRLYDEKQOHVHCSNDLLGDLFGVPSPVSKHRKIYTMIR 89

Db 77 PKVLDLQVLFYLGQYIMTKRLYDEKQOHVHCSNDLLGDLFGVPSPVSKHRKIYTMIR 136

Qy 90 NLVVNQESSDSGTSVSEN 109

Db 137 NLVVNQESSDSGTSVSEN 156

# RESULT 10

US-10-287-226-382  
 ; Sequence 382, Application US/10287226  
 ; Publication No. US20040086875A1

## GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,  
 ; APPLICANT: Alsobrook, John P.,  
 ; APPLICANT: Berghs, Constance,  
 ; APPLICANT: Boldog, Ference,  
 ; APPLICANT: Burgess, Catherine E.,  
 ; APPLICANT: Chant, John S.,  
 ; APPLICANT: Chaudhuri, Amitabha,  
 ; APPLICANT: DiPippo, Vincent A.,  
 ; APPLICANT: Edinger, Shlomit R.,  
 ; APPLICANT: Eisen, Andrew,  
 ; APPLICANT: Ellerman, Karen,  
 ; APPLICANT: Gangolli, Esha A.,  
 ; APPLICANT: Gorman, Linda,  
 ; APPLICANT: Gerlach, Valerie,  
 ; APPLICANT: Ji, Weizhen,  
 ; APPLICANT: Kekuda, Ramesh,  
 ; APPLICANT: Khrantsov, Nikolai,  
 ; APPLICANT: Li, Li,  
 ; APPLICANT: Malyankar, Uriel M.,  
 ; APPLICANT: MacDougall, John R.,  
 ; APPLICANT: Mezes, Peter S.,  
 ; APPLICANT: Millet, Charles E.,  
 ; APPLICANT: Millet, Isabelle,  
 ; APPLICANT: Ooi, Chean Eng,  
 ; APPLICANT: Ort, Tatiana,  
 ; APPLICANT: Padigaru, Muralidhara,



```
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca, K.,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderina, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 382
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-226-382

Query Match      94.3%; Score 522.5; DB 15; Length 522;
Best Local Similarity 77.1%; Pred. No. 3.3e-53;
Matches 108; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

Qy      1  SOIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKE----- 36
Db      17  SOIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEWSFTMLPRLVWNSWAQGICLPRP 76
Qy      37  -----VLFYLGQVIMTKRLYDEKQOHHVHCNSDLLGDLFGVPSFSVKEHRKIYTMILYR 89
Db      77  PKVLDQLVFLYLGQVIMTKRLYDEKQOHHVHCNSDLLGDLFGVPSFSVKEHRKIYTMILYR 136
Qy      90  NLVVVWVQSSDSGTSVSEN 109
Db      137  NLVVVWVQSSDSGTSVSEN 156

RESULT 11
US-09-956-425-6
; Sequence 6, Application US/09956425
; Patent No. US20020045192A1
; GENERAL INFORMATION:
; APPLICANT: Kriwacki, Richard
; APPLICANT: Bothner, Brian
; APPLICANT: Lewis, William
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof
; FILE REFERENCE: 1340/1/035
; CURRENT APPLICATION NUMBER: US/09/956,425
; CURRENT FILING DATE: 2001-09-19
```

```
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-956-425-6

Query Match      88.2%; Score 488.5; DB 9; Length 489;
Best Local Similarity 87.2%; Pred. No. 3.3e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;

Qy      1  SOIPASQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQVIMTKRLYDEKQOHHVH 60
Db      17  SOIPASQETLVRPKPLLLKLLKSVGAQNDYTMKEIIFYIGQVIMTKRLYDEKQOHHIV 76
Qy      61  CSNDLLGDLFGVPSFSVKEHRKIYTMILYRNVLVVWVQSSDSGTSVSEN 109
Db      77  CSNDLLGDLFGVPSFSVKEHRKIYMIYRNVLVAVSQ---DSGTSLS 122

RESULT 12
US-09-966-724-4
; Sequence 4, Application US/09966724
; Publication No. US20040170971A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,724
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/044,619
; FILING DATE: 2001-10-01
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMB UT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-966-724-4

Query Match      88.2%; Score 488.5; DB 11; Length 489;
Best Local Similarity 87.2%; Pred. No. 3.3e-49;
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;
```

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVH 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTMKEIIIFYIGQYIMTKRLYDEKQOHHIVY 76  
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVNQESSDSGTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYAMIRNLLVAVSQ---DSGTSLSSES 122

RESULT 13  
US-10-685-838-2  
; Sequence 2, Application US/10685838  
; Publication No. US20040197893A1  
; GENERAL INFORMATION:  
; APPLICANT: SHUBERT, CARSTEN  
; APPLICANT: GRASBERGER, BRUCE  
; APPLICANT: MAGUIRE, DIANE  
; APPLICANT: DECKMAN, INGRID  
; APPLICANT: SPURLINO, JOHN  
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
; FILE REFERENCE: PRD-2137-USANP  
; CURRENT APPLICATION NUMBER: US/10/685,838  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/418,350  
; PRIOR FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-685-838-2

Query Match 86.8%; Score 481; DB 16; Length 95;  
Best Local Similarity 98.9%; Pred. No. 3e-49;  
Matches 94; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVH 60  
Db 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVY 60  
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVVN 95  
Db 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVVN 95

RESULT 14  
US-10-685-838-4  
; Sequence 4, Application US/10685838  
; Publication No. US20040197893A1  
; GENERAL INFORMATION:  
; APPLICANT: SHUBERT, CARSTEN  
; APPLICANT: GRASBERGER, BRUCE  
; APPLICANT: MAGUIRE, DIANE  
; APPLICANT: DECKMAN, INGRID  
; APPLICANT: SPURLINO, JOHN  
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
; FILE REFERENCE: PRD-2137-USANP  
; CURRENT APPLICATION NUMBER: US/10/685,838  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/418,350  
; PRIOR FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 4  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-685-838-4

Query Match 85.2%; Score 472; DB 16; Length 95;  
Best Local Similarity 97.9%; Pred. No. 3.5e-48;  
Matches 93; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVH 60  
Db 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVY 60  
Qy 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVVN 95  
Db 61 CSNDLLGDLFGVPSFSVKEHRKIYTMIRNLLVVVN 95

RESULT 15  
US-10-685-838-3  
; Sequence 3, Application US/10685838  
; Publication No. US20040197893A1  
; GENERAL INFORMATION:  
; APPLICANT: SHUBERT, CARSTEN  
; APPLICANT: GRASBERGER, BRUCE  
; APPLICANT: MAGUIRE, DIANE  
; APPLICANT: DECKMAN, INGRID  
; APPLICANT: SPURLINO, JOHN  
; TITLE OF INVENTION: HDM2-INHIBITOR COMPLEXES AND USES THEREOF  
; FILE REFERENCE: PRD-2137-USANP  
; CURRENT APPLICATION NUMBER: US/10/685,838  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR APPLICATION NUMBER: 60/418,350  
; PRIOR FILING DATE: 2002-10-16  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 3  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-685-838-3

Query Match 84.5%; Score 468; DB 16; Length 92;  
Best Local Similarity 98.9%; Pred. No. 1e-47;  
Matches 91; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 EQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVHCSNDLL 66  
Db 1 EQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHHIVCSNDLL 60  
Qy 67 GDLFGVPSFSVKEHRKIYTMIRNLLVVVNQOE 98  
Db 61 GDLFGVPSFSVKEHRKIYTMIRNLLVVVNQOE 92

Search completed: February 16, 2005, 08:50:04  
Job time : 698 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 38 Seconds  
(without alignments)  
275.990 Million cell updates/sec

Title: US-10-822-254-6  
Perfect score: 554  
Sequence: 1 SQIPASEQETLVRPKPLLLK.....NLVVNQESSDSGTSVSEN 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	98.9	491	1 S24354	p53-binding protei
2	488.5	88.2	489	2 S15349	mdm2 protein - mou
3	271.5	49.0	489	2 S71955	MDM2-like p53-bind
4	84	15.2	685	1 SXBPT4	NAD+-protein ADP-r
5	84	15.2	698	1 S31630	NAD+-protein ADP-r
6	84	15.2	698	1 S31714	NAD+-protein ADP-r
7	73.5	13.3	467	2 T25848	hypothetical prote
8	72.5	13.1	565	2 S52682	hypothetical prote
9	72.5	13.1	2833	2 A43360	inositol 1,4,5-tri
10	72	13.0	967	2 A64710	type III restricti
11	71.5	12.9	514	2 D85069	hypothetical prote
12	70.5	12.7	709	2 E64213	DNA topoisomerase
13	70.5	12.7	838	2 I45557	eyeless, long form
14	70	12.6	969	2 E71810	type III restricti
15	68	12.3	134	2 G69382	response regulator
16	67	12.1	176	2 J01813	B19R protein - vac
17	67	12.1	181	2 S75415	probable ribosomal
18	67	12.1	261	2 H71680	exodeoxyribonuclea
19	67	12.1	3092	2 S46009	GTPase-activating
20	66.5	12.0	422	2 T26334	hypothetical prote
21	66.5	12.0	447	2 I64002	sodium-translocat
22	66.5	12.0	517	2 S32169	hypothetical prote
23	65.5	11.8	277	2 A10589	conserved hypothet
24	65.5	11.8	339	2 A90395	conserved hypothet
25	65.5	11.8	425	2 T50184	mammalian swi/snf
26	65.5	11.8	450	2 G70210	conserved hypothet
27	65.5	11.8	704	2 H82381	toxin secretion AT
28	65	11.7	232	2 E82501	hypothetical prote
29	65	11.7	260	2 T28182	hypothetical prote

30	64.5	11.6	331	2 B84938	flagellar motor sw
31	64.5	11.6	525	2 T15185	hypothetical prote
32	64	11.6	286	2 B97743	exodeoxyribonuclea
33	64	11.6	316	2 F69491	methenyltetrahydro
34	64	11.6	346	2 G72094	ct244 hypothetical
35	64	11.6	346	2 G86528	CT244 hypothetical
36	64	11.6	346	2 B81574	conserved hypothet
37	64	11.6	369	2 B70220	conserved hypothet
38	64	11.6	488	2 T47943	1-aminocyclopropan
39	64	11.6	600	2 H81733	DNA primase TC0175
40	64	11.6	855	2 B89472	protein ZC53.4 (im
41	64	11.6	860	2 S64366	hypothetical prote
42	64	11.6	908	2 C70168	DNA polymerase I (
43	64	11.6	1026	2 C71490	probable exodeoxyr
44	63.5	11.5	353	2 D69001	conserved hypothet
45	63.5	11.5	366	2 T07827	1-aminocyclopropan

## ALIGNMENTS

## RESULT 1

S24354  
p53-binding protein mdm2 - human  
N:Alternate names: mdm-2 oncogene; mouse double minute 2 homolog; p53-associated phosph  
N:Contains: p53-binding protein mdm2, splice form A  
C:Species: Homo sapiens (man)  
C:Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000  
C:Accession: S24354; S57338; G02026  
R:Oliner, J.D.; Kinzler, K.W.; Meltzer, P.S.; George, D.L.; Vogelstein, B.  
Nature 358, 80-83, 1992  
A:Title: Amplification of a gene encoding a p53-associated protein in human sarcomas.  
A:Reference number: S24354; MUID:92310576; PMID:1614537  
A:Accession: S24354  
A:Molecule type: mRNA  
A:Residues: 1-491 <OLI>  
A:Cross-references: EMBL:Z12020; NID:G35211; PIDN:CAA78055.1; PID:G35212  
R:Zauberman, A.; Flusberg, D.; Haupt, Y.; Barak, Y.; Oren, M.  
Nucleic Acids Res. 23, 2584-2592, 1995  
A:Title: A functional p53-responsive intronic promoter is contained within the human mdm  
A:Reference number: S57338; MUID:95380270; PMID:7651818  
A:Accession: S57338  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-16,'P',18-24 <ZAU>  
A:Cross-references: EMBL:U28935; NID:G904033; PIDN:AAA82237.1; PID:G904034  
R:Lunec, J.  
submitted to the EMBL Data Library, August 1995  
A:Description: Multiple alternate spliced mdm2 transcripts with loss of p53 binding dom  
A:Reference number: G09070  
A:Accession: G02026  
A:Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-27,223-491 <LUN>  
A:Cross-references: EMBL:U33199; NID:G992676; PIDN:AAA75514.1; PID:G992677  
A:Experimental source: splice form A  
C:Genetics:  
A:Gene: GDB:MDM2  
A:Cross-references: GDB:250456; OMIM:164785  
A:Map position: 12q14.3-12q15  
C:Superfamily: human p53-binding protein mdm2  
C:Keywords: alternative splicing; oncogene; phosphoprotein  
F:1-491/Product: p53-binding protein mdm-2 #status predicted <MAT1>  
F:1-27,223-491/Product: p53-binding protein mdm-2, splice form A #status predicted <MAT1>

Query Match 98.9%; Score 548; DB 1; Length 491;

Best Local Similarity 99.1%; Pred. No. 5e-49; Indels 0; Gaps 0;  
Matches 108; Conservative 1; Mismatches 0;

QY 1 SQIPASEQETLVRPKPLLLKLSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHVH 60  
|||||  
DB 17 SQIPASEQETLVRPKPLLLKLSVGAQKDYTMKEVLFYLGQYIMTKRLYDEKQOHVY 76  
|||||

Qy	61	C S N D L L G D L F G V P S V K E H R K I Y T M I Y R N L V V V N Q Q E S D S D S G T S V S E N	109
Db	77	C S N D L L G D L F G V P S V K E H R K I Y T M I Y R N L V V V N Q Q E S D S D S G T S V S E N	125

## RESULT 2

S15349  
mdm2 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S15349  
R:Rakharzadeh, S.S.; Trusko, S.P.; George, D.L.  
EMBO J. 10, 1565-1569, 1991.  
A;Title: Tumorigenic potential associated with enhanced expression of a gene that is amplified in human bladder cancer.  
A;Reference number: S15349; MID:91224107; PMID:2026149  
A;Accession: S15349  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-489 <PAK>  
A;Cross-references: UNIPROT:P3804; EMBL:X58876; NID:g53038; PID:CAA41684.1; PID:g53038  
C;Genetics:  
A;Gene: mdm2  
C;Superfamily: human p53-binding protein mdm2

Query Match 88.2%; Score 488.5; DB 2; Length 489;  
Best Local Similarity 87.2%; Pred. No. 7.4e-43;  
Matches 95: Conservative 8; Mismatches 3; Indels 3.

QY 1 SQIPASEQETLVRPXPPLLLKLLKSVGAQKDTYTMKEVLFYLGQVIMTKRLYDEKQOHVH 60  
 |||||  
 Db 17 SQIPASEQETLVRPXPPLLLKLLKSVGAQNDTYTMKEITFYIGAVIMTKRLYDEKQOHIV 76  
 |||||

**Qy** 61 CSNDLLGDLFGVPSPSVKEHRKIYTMIRNLVVNQESDSDSGTSVSEN 109  
|||||:|||||:|||||:|||||:|||||:  
**Db** 77 CSNDLLGDVEGVPSFSVKEHRTKIVMTVNTAVSQO---DSCTSTSES 123

### RESULT 3

S71955  
MDM2-like p53-binding protein MDMX - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C:Accession: S71955  
R:Shvarts, A.; Steegenga, W.T.; Riteco, N.; van Laar, T.; Dekker, P.; Barzuine, M.; van H  
EMBO J. 15, 5349-5357, 1996  
A:Title: MDMX: a novel p53-binding protein with some functional properties of MDM2.  
A:Reference number: S71955; MUID:97050840; PMID:8895579  
A:Accession: S71955  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-489 <SHV>  
A:Cross-references: UNIPROT:O35618; EMBL:AF007110; NID:g2253388; PIDN:AAB62927.1; PID:g2  
C:Genetics:  
A:Gene: MDMX  
C:Function:  
A:Description: inhibits transcription activation function of tumour suppressor protein p  
C:Superfamily: human p53-binding protein mdm2

Query Match	49.0%;	Score 271.5;	DB 2;	Length 489;
Best Local Similarity	52.4%;	Pred. No. 2.4e-20;		
Matches	55: Conservative	17: Mismatches	22: Indels	11: Gaps

[illegible]

QY 65 LLGDLFGVPFSVKEHRKIYTMIRNLVVNQESSDSTGTSVSEN 109  
||||| | ||||| : | : |||  
db 80 LLGDLFGCOSFSVKQSPSPVMIKNIY-----TSASNNY 112

**RESULT 4**  
**SXBPT4**

NAD<sup>+</sup>-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T4  
 C;Species: phage T4  
 A;Note: host *Escherichia coli*  
 C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
 C;Accession: J00096  
 R;Hilse, D.; Koch, T.; Rueger, W.  
 Nucleic Acids Res. 17, 6731, 1989  
 A;Title: Nucleotide sequence of the alt gene of bacteriophage T4.  
 A;Reference number: J00096; MUID:89386005; PMID:2506556  
 A;Accession: J00096  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-685 <HIL>  
 A;Cross-references: UNIPROT:P12726  
 C;Comment: This enzyme catalyzes the ADP-ribosylation of one of the two alp  
 C;Genetics:

```

Query Match      15.2%; Score 84; DB 1; Length 685;
Best Local Similarity 29.0%; Pred. No. 0.98;
Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6

Qy 18 LKLLKRS--VGAQKDITVTMEKVFYLL---QQYIMTKEL--YDEKQOHI-VHCNSDNLGLD 69
      |||:|||||
Db 111 MLRLKSKTAGAARQIOVIADRLIRSGRGYVLLKELWDYDKYAVILHRKNVSLDI 170

```

**QY** 70 FGVPFSVKEHRKIYTMIRNLVVNQESSDSGTSVSEN 109  
||| | : : : | : :  
**D6** 174 PGVPEISTELFTKVESKV--GDVYINK----DTGAOVTKN 204

## RESULT 5

S31630  
NAD+-protein ADP-ribosyltransferase (EC 2.4.2.-) precursor - phage T2  
C/Species: phage T2  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C/Accession: S31630  
R/Koch, T.; Rueger, W.  
A/Submitted to the EMBL Data Library, December 1992  
A/Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6:  
A/Reference number: S31630  
A/Accession: S31630  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-698 <KOC>  
A/Cross-references: UNIPROT:Q38424; EMBL:X69893; NID:g15187; PIDN:CAA49517;  
C/Superfamily: phage T4 NAD-protein ADP-ribosyltransferase  
C/Keywords: glycosyltransferase; NAD; pentosyltransferase

Query Match	15.2%	Score 84;	DB 1;	Length 698;
Best Local Similarity	29.0%;	Pred. No. 1;		
Matches	29;	Conservative	22;	Mismatches 35;
				Indels 14;
				Gaps 6;

18	LKLLKS--VGAQKDVTYMEVLPYL---QOYIMTKEL--YDSKQOHI-VHCSDNLLGLD	69
QY		
112	MLRLIKSTAGCAQARQIQVIADRLIRSGGRYVLLKELWDYDKKYAYILIHKNVSLDI	171
DB		
70	FGVPSFSVKEHRKIYTIWIRNLVVVNQESSDSCTSVSEN	109
QY		
172	PGVPEISITELTKVESKV--GDVYINK---DTGAOYTKN	205
DB		

## RESULT 6

S31714  
NAD<sup>+</sup>-protein ADP-riboseyltransferase (EC 2.4.2.-) precursor - phage T6  
C-species: Phage T6  
C-date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C-accession: S31714  
R.Koch, T. J. Rueger, W.  
submitted to the EMBL Data Library, December 1992

```

A;Description: The ADP-ribosyltransferase of bacteriophages T2, T4 and T6: Sequencing of
A;Reference number: S31630
A;Accession: S31714
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-698 <KOC>
A;Cross-references: UNIPROT:Q38433; EMBL:X69894; NID:g15422; PIDN:CAA49518.1; PID:g15423
C;Superfamily: phage T4 NAD-protein ADP-ribosyltransferase
C;Keywords: glycosyltransferase; NAD; pentosyltransferase

      Query Match          15.2%; Score 84; DB 1; Length 698;
      Best Local Similarity 29.0%; Pred.No. 1;
      Matches 29; Conservative 22; Mismatches 35; Indels 14; Gaps 6;

QY   18 LLKLKLS--VGAQKDTYTWKVELFYLV---GQYIMTKRL--YDEKQQQH-VHCNSNDLLGLD 69
     :::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   112 MLRIILSKTAGAQIQVIADRLIRSRSGRYVLKKELNDYDKKYAVILHRRKNVSLEDI 171
           ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY   70 GFVPSPSVKEHRKIYMIYRNVLVVNQSSSDSGTGSVEN 109
     ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   172 PGVPEISTELTFVESKV--GDVYINK---DTGAQVTKN 205
           ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
T25848
hypothetical protein T01B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25848
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25848
A;Status: preliminary; translated from GB/EMBL/DDBBJ
A:Molecule type: DNA
A;Residues: 1-467 <GEI>
A;Cross-references: UNIPROT:P91408; EMBL:U80931; PIDN:AAB37999.1; GSPDB:GN000022; CESP:T2
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Gene: CESP.T01B11.2
A;Map position: 4
A;Antons: 39/2; 79/1; 131/2; 156/2; 337/3; 389/2
C;Superfamily: ornithine-oxo-acid aminotransferase

      Query Match          13.3%; Score 73.5; DB 2; Length 467;
      Best Local Similarity 32.9%; Pred.No. 7.7;
      Matches 25; Conservative 5; Mismatches 25; Indels 21; Gaps 3;

QY   1 SQIPASEQETLVRPKPILLKLSVGQAQKDITYTWKELVFYLGQYIMTKR-----LYDEKQ 55
     |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   13 SSTPAAATKDVRSKEILK-----RRKDTISGCKQIFYSDDPFMVVRASMQYLDEKS 66
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY   56 -----OHIVHC 61
     ||::|::|
Db   67 NKFLDCITSNVQHVGHG 82
           ||::|

RESULT 8
S52682
hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52682
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Accession: S52682
A:Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q04600; EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN000004
C;Genetics:

```

```
Query Match      13.0%; Score 72; DB 2; Length 967;
Best Local Similarity 24.8%; Pred. No. 26;
Matches 26; Conservative 21; Mismatches 44; Indels 14; Gaps 3;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQOH 57
DB 768 NEIKNEQEGRLRUELEFLIYIYQNIKDYSQMRIT---IKNRKDAFYDEKGEI 821

QY 58 IVHCSNDLLGDLFGVPSFSVKEHRKIYTMIVRNVLVVNQESSDS 102
DB 822 REFLDGLGADKADYKIKNSSVRE-----KCLYENFMQVDSEIEKOT 861

RESULT 11
D85069
hypothetical protein AT4G05520 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85069
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
  Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85069
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <STO>
A:Cross-references: UNIPROT:Q9S9W1; GB:NC_001268; NID:g7267312; PIDN:CAB81094.1; GSPDB:C
C:Genetics:
A:Gene: AT4G05520
A:Map position: 4

Query Match      12.9%; Score 71.5; DB 2; Length 514;
Best Local Similarity 29.7%; Pred. No. 14;
Matches 27; Conservative 13; Mismatches 26; Indels 25; Gaps 4;

QY 15 KPILLKLLKSVGA-----QKDTYTMKEVLFYLGQY-----IMTKLYDEKQOH 58
DB 384 QPLFLKLMRYGALMWSLKGVLNTPVVRVYIGSFNDKPNVAVGPICKELFEKEQ--- 440

QY 59 VHCNSDILLGDLFGVPSFSVKEHRKIYTMIVR 89
DB 441 ----NDLLADLMDVPKKAC--DRKINEFVKR 465

RESULT 12
E64213
DNA topoisomerase (EC 5.99.1.2) - Mycoplasma genitalium
N:Alternate names: type I DNA topoisomerase
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: E64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
  M.; Fuhrmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
  C.A.; Venter, J.C.
  Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: E64213
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-709 <TIGR>
A:Cross-references: UNIPROT:P47368; GB:U39691; GB:L43967; NID:g1045794; PID:g1045802; TI
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: DNA topoisomerase I
C:Keywords: isomerase

Query Match      12.7%; Score 70.5; DB 2; Length 709;
Best Local Similarity 23.4%; Pred. No. 26;
Matches 22; Conservative 18; Mismatches 45; Indels 9; Gaps 2;
```

```
QY 21 LLKSVGAQKDTYTMKEVLFYLGQYIMTKLYDE-----KQOHVHCNSDILLGDLFGVPSF 75
DB 431 IVFINKNKFTYSSKSLFDGY---QRLYEIKNTKDELIDLSKLKIGKFSFEKI 486

QY 76 SVKEHRKIYTMIVRNVLVVNQESSDSCTSUSEN 109
DB 487 SVNEHKTNPFPYTOASLIEELEKSNIGRPSTYN 520

RESULT 13
I45557
eyeless, long form - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 16-Aug-2004
C:Accession: I45557
R:Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
  Science 265, 785-789, 1994
A:Title: Homology of the eyeless gene of Drosophila to the Small eye gene in mice and An
A:Reference number: A54584; MUID:94323757; PMID:7914031
A:Accession: I45557
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-838 <RES>
A:Cross-references: EMBL:X79493; NID:g641809; PIDN:CAA56038.1; PID:g641810
C:Genetics:
A:Gene: FlyBase:ey
A:Cross-references: FlyBase:FBgn0005558
A:Introns: 37/1; 92/3; 152/3; 371/1; 429/1; 521/1; 639/2
C:Superfamily: homeobox homology; paired box homology
C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F:37-161/Domain: paired box homology <PBH>
F:412-468/Domain: homeobox homology <HOX>

Query Match      12.7%; Score 70.5; DB 2; Length 838;
Best Local Similarity 26.0%; Pred. No. 31;
Matches 26; Conservative 14; Mismatches 33; Indels 27; Gaps 5;

QY 12 VRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQY-----IMTKLYDEKQOHVHCNSDL 65
DB 99 IRP-----RAITGSKPRVATAEVVSKISQYKRECFSAWEIRDRLQENV-CTND- 148

QY 66 LGDLFGVPSFSVKEHRKIYTMIVRNVLVVNQESSDSGTS 105
DB 149 -----NIPSVS-----SINRVLRLAAQKEQQSGSGSS 177

RESULT 14
E71810
type III restriction enzyme - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: E71810
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
  Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
  Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: E71810
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-969 <ARN>
A:Cross-references: UNIPROT:Q9ZJA3; GB:AE001563; GB:AE001439; NID:g4156027; PIDN:RAD0698
A:Experimental source: strain J99
C:Genetics:
A:Gene: res_2

Query Match      12.6%; Score 70; DB 2; Length 969;
Best Local Similarity 22.9%; Pred. No. 41;
Matches 24; Conservative 20; Mismatches 47; Indels 14; Gaps 3;

QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKR---LYDEKQOH 57
DB 768 NEIKNEQEGRLRUELEFLIYIYQNIKDYSQMRIT---IKNRKDAFYDEKGEI 821
```

Db 770 NEIKKNEQGLRLLEFLLEIIYQNIKOKISYQMBETT-----IKNRKNDAFYDEKGE- 822

QY 58 IVHCNNDLLGLDGLFGVPSPSVKHKRIYTIYTNLVVNNQESSDS 102

Db 823 ----IREFLDGLGADKVEIKNSSAQEKCLYENFMQVDSEIEKDT 863

# RESULT 15

G69382  
 response regulator homolog - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: G69382  
 R.; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Accession: G69382  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-134 <KLE>  
 A:Cross-references: UNIPROT:Q29199; GB:AE001029; GB:AE000782; NID:92689352; PIDN:AB9017  
 C:Superfamily: signal transduction receiver (phosphoacceptor) protein, Chey type; respon  
 C:Keywords: phosphoprotein  
 F:20-126/Domain: response regulator homology <RRH>  
 P:66/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 12.3%; Score 68; DB 2; Length 134;  
 Best Local Similarity 28.4%; Pred. No. 6.8;  
 Matches 21; Conservative 15; Mismatches 38; Indels 0; Gaps 0;

QY 35 KEVLFLVGYIMTKRLYDEKQKHVHCNNDLLGLDGLFGVPSPSVKHKRIYTIYTNLVV 94

Db 6 KFLFWLHPNIMTKILVDDDCSICELYKILGSFEVWSACSGREGLELYRKIMPDLVIV 65

QY 95 NQESSSDSGTSVSE 108

Db 66 DINMPDISGVEVAK 79

Search completed: February 16, 2005, 08:24:51  
 Job time : 41 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2005, 08:21:05 ; Search time 170 Seconds

(without alignments)  
328.333 Million cell updates/sec

Title: US-10-822-254-6

Perfect score: 554

Sequence: 1 SQIPASEQETLVLRPKPLLLK.....NLVVNQSSDSTSVSEN 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	548	98.9	166	Q8NDW2	Q8ndw2 homo sapien
2	548	98.9	195	Q96DS4	Q96ds4 homo sapien
3	548	98.9	243	Q8TE47	Q8te47 homo sapien
4	548	98.9	491	1 MDM2_HUMAN	Q00987 homo sapien
5	536	96.8	487	1 MDM2_CANPA	P56950 canis famil
6	536	96.8	487	2 Q9GMZ6	Q9gmz6 canis famil
7	536	96.8	491	1 MDM2_HORSE	P56951 equus cabal
8	533	96.2	491	2 Q7YRZ8	Q7yrz8 felis silve
9	498	88.9	436	2 Q8WYJ2	Q8wyj2 homo sapien
10	488.5	88.2	489	1 MDM2_MOUSE	P23804 mus musculus
11	488.5	88.2	489	2 Q91XK7	Q91xk7 m mus muscu
12	471	85.0	118	2 Q8WYJ3	Q8wyj3 homo sapien
13	464.5	83.8	466	1 MDM2_MESAU	Q60524 mesocricetu
14	421	76.0	325	2 Q8TE46	Q8te46 homo sapien
15	402	72.6	173	2 Q8TE46	Q8te46 homo sapien
16	364	65.7	473	1 MDM2_XENLA	P56273 xenopus lae
17	364	65.7	473	2 Q6GMB5	Q6gmb5 xenopus lae
18	363	65.5	482	2 Q6P3Q9	Q6p3q9 xenopus tro
19	334	60.3	105	2 Q8NDW0	Q8ndw0 homo sapien
20	315	56.9	426	2 Q9GK41	Q9gk41 canis famil
21	298.5	53.9	445	1 MDM2_BRARE	Q42354 brachydanio
22	280.5	50.6	446	2 Q8WYJ1	Q8wyj1 homo sapien
23	274	49.5	491	2 Q7ZUW7	Q7zuw7 brachydanio
24	272	49.1	475	2 Q7ZV13	Q7zv13 xenopus lae
25	271.5	49.0	489	1 MDM4_MOUSE	Q35618 mus musculus
26	268.5	48.5	489	2 Q9CYG1	Q9cyg1 m mus muscu
27	262	47.3	490	2 Q99L86	Q99l86 mus musculus
28	260.5	47.0	134	2 Q6PHL8	Q6phl8 xenopus lae
29	246	44.4	140	2 Q68DC0	Q68dc0 homo sapien
30	246	44.4	153	2 Q6MZR7	Q6mzr7 homo sapien
31	244	44.0	490	1 MDM4_HUMAN	O15151 homo sapien

32	223	40.3	69	2	Q86WA4	Q86wa4 homo sapien
33	216	39.0	66	2	Q86DS3	Q86ds3 homo sapien
34	213	38.4	70	2	Q86WA3	Q86wa3 homo sapien
35	199	35.9	95	2	Q96DS1	Q96ds1 homo sapien
36	179.5	32.4	70	2	Q8NDW1	Q8ndw1 homo sapien
37	177	31.9	159	2	Q96DS0	Q96ds0 homo sapien
38	176	31.8	60	2	Q96DS5	Q96ds5 homo sapien
39	176	31.8	130	2	Q9H4C3	Q9h4c3 homo sapien
40	176	31.8	243	2	Q9H4C5	Q9h4c5 homo sapien
41	175	31.6	65	2	Q86WA5	Q86wa5 homo sapien
42	156	28.2	50	2	Q8NDV9	Q8ndv9 homo sapien
43	119.5	21.6	54	2	Q86WA2	Q86wa2 homo sapien
44	84.5	15.3	1132	2	O40913	O40913 human herpe
45	84	15.2	682	1	ALT_BPT4	P12726 bacterioph

#### ALIGNMENTS

##### RESULT 1

Q8NDW2 PRELIMINARY; PRT; 166 AA.  
 AC Q8NDW2;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE P53-binding protein.  
 DE P53-binding protein.  
 GN Name=MDM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AJ491698; CAD36959.1; -;  
 DR HSSP; Q9UMR8; IYCR.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB\_MDM2.  
 DR Pfam; PF02201; SWIB; 1.  
 SQ SEQUENCE 166 AA; 18900 MW; FA6B5BA18E85040D CRC64;

Query Match 98.9%; Score 548; DB 2; Length 166;  
 Best Local Similarity 99.1%; Pred. No. 7.1e-51;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVLRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVH 60

DB 17 SQIPASEQETLVLRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDFGVPSFVKEHRKIYTMIVRNLVVNVNQSSDSTSVSEN 109

DB 77 CSNDLLGLDFGVPSFVKEHRKIYTMIVRNLVVNVNQSSDSTSVSEN 125

##### RESULT 2

Q96DS4 PRELIMINARY; PRT; 195 AA.  
 AC Q96DS4;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE MDM2 variant FB26.  
 DE MDM2 variant FB26.  
 GN Name=MDM2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Rhabdomyosarcoma tumor;

QY 61 CSNDLLGLDFGVPSFVKEHRKIYTMIVRNLVVNVNQSSDSTSVSEN 109

DB 77 CSNDLLGLDFGVPSFVKEHRKIYTMIVRNLVVNVNQSSDSTSVSEN 125

RA Bartel F., Taylor A.C., Taubert H., Harris L.C.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF385323; AAL13243.1; -;  
DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

SQ SEQUENCE 195 AA; 22161 MW; 4987AE567DB12D5D CRC64;

Query Match 98.9%; Score 548; DB 2; Length 195;  
Best Local Similarity 99.1%; Pred. No. 8.5e-51;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPFSVKEHRKIYTWIYRNLVVNVNQESSDSGTSVSEN 109

Db 77 CSNDLLGLDGLFGVPFSVKEHRKIYTWIYRNLVVNVNQESSDSGTSVSEN 125

## RESULT 3

Q8TE47 PRELIMINARY; PRT; 243 AA.

AC Q8TE47;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MDM2 isoform KB9 protein.

GN Name=MDM2 isoform KB9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphocytes;

RA Bartel F., Pinkert D., Kappeler M., Bache M., Schmidt H., Taubert H.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ340612; CND23251.1; -;

DR HSP; Q9UMT8; 1YCR.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; F:protein ubiquitination; IEA.

DR InterPro; IPR010984; MDM2.

DR InterPro; IPR003121; SWIB\_MDM2.

DR Pfam; PF02201; SWIB; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF\_RING\_2; 1.

SQ SEQUENCE 243 AA; 27317 MW; 9EB5D0142CF185A2 CRC64;

Query Match 98.9%; Score 548; DB 2; Length 243;  
Best Local Similarity 99.1%; Pred. No. 1.1e-50;  
Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVH 60

Db 17 SQIPASEQETLVRPRLKLLKLSVGAQKDTYTMKEVLVFLGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPFSVKEHRKIYTWIYRNLVVNVNQESSDSGTSVSEN 109

Db 77 CSNDLLGLDGLFGVPFSVKEHRKIYTWIYRNLVVNVNQESSDSGTSVSEN 125

## RESULT 4

MDM2\_HUMAN

ID\_MDM2\_HUMAN STANDARD; PRT; 491 AA.

AC Q00987; Q13226; Q13297; Q13298; Q13299; Q13300; Q13301; Q9UGI3;

AC

DT

DT

DT

DE

DE

GN

OS

OC

OC

OX

RN

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

RC

RA

RT

RT

RL

RL

RP

Q9UMT8;

01-APR-1993 (Rel. 25, Created)

01-APR-1993 (Rel. 25, Last sequence update)

25-OCT-2004 (Rel. 45, Last annotation update)

Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein

Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Hdm2).

Name=MDM2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI\_TaxID=9606;

[1] SEQUENCE FROM N.A. (ISOFORM MDM2).

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

MDM2

SEQUENCE OF 1-24 FROM N.A.  
 MEDLINE=95380270; PubMed=7651818;  
 Zauberman A., Flusberg D., Haupt Y., Barak Y., Oren M.;  
 "A functional p53-responsive intronic promoter is contained within the  
 human mdm2 gene.";  
 Nucleic Acids Res. 23:2584-2592(1995).  
 [8]  
 RP  
 SEQUENCE OF 1-9 FROM N.A.  
 MEDLINE=97413643; PubMed=9270029;  
 Landers J.B., Cassel S.L., George D.L.;  
 "Translational enhancement of mdm2 oncogene expression in human tumor  
 cells containing a stabilized wild-type p53 protein.";  
 Cancer Res. 57:3562-3568(1997).  
 [9]  
 RP  
 SEQUENCE OF 301-481 FROM N.A.  
 MEDLINE=20542019; PubMed=11087894; DOI=10.1016/S0027-5107(00)00112-3;  
 Taubert H., Kappler M., Meyer A., Bartel F., Schlott T.,  
 Lautenschlaeger C., Bache M., Schmidt H., Wuerl P.;  
 "A MboII polymorphism in exon 11 of the human MDM2 gene occurring in  
 normal blood donors and in soft tissue sarcoma patients: an indication  
 for an increased cancer susceptibility?";  
 Mutat. Res. 456:39-44(2000).  
 [10]  
 RP  
 MUTAGENESIS OF CYS-464.  
 MEDLINE=98111004; PubMed=9450543; DOI=10.1016/S0014-5793(97)01480-4;  
 Honda R., Tanaka H., Yasuda H.;  
 "Oncoprotein MDM2 is a ubiquitin ligase E3 for tumor suppressor p53.";  
 FEBS Lett. 420:25-27(1997).  
 [11]  
 RP  
 MUTAGENESIS OF CYS-449.  
 MEDLINE=20190101; PubMed=10723139; DOI=10.1038/sj.onc.1203464;  
 Honda R., Yasuda H.;  
 "Activity of MDM2, a ubiquitin ligase, toward p53 or itself is  
 dependent on the RING finger domain of the ligase.";  
 Oncogene 19:1473-1476(2000).  
 [12]  
 RP  
 MUTAGENESIS.  
 MEDLINE=20187618; PubMed=10722742; DOI=10.1074/jbc.275.12.8945;  
 Fang S., Jensen J.P., Ludwig R.L., Vousden K.H., Weissman A.M.;  
 "Mdm2 is a RING finger-dependent ubiquitin protein ligase for itself  
 and p53.";  
 J. Biol. Chem. 275:8945-8951(2000).  
 [13]  
 RP  
 MUTAGENESIS OF CYS-441 AND CYS-478.  
 MEDLINE=20076498; PubMed=10608892; DOI=10.1074/jbc.274.53.38189;  
 Sharp D.A., Kratowicz S.A., Sank M.J., George D.L.;  
 "Stabilization of the MDM2 oncoprotein by interaction with the  
 structurally related DMX protein.";  
 J. Biol. Chem. 274:38189-38196(1999).  
 [14]  
 RP  
 NUCLEOLAR LOCALIZATION SIGNAL.  
 MEDLINE=20173879; PubMed=10707090; DOI=10.1038/35004057;  
 Lohrum M.A.E., Aehcroft M., Kubbutat M.H.G., Vousden K.H.;  
 "Identification of a cryptic nucleolar-localization signal in MDM2.";  
 Nat. Cell Biol. 2:179-181(2000).  
 [15]  
 RP  
 PHOSPHORYLATION BY ATM.  
 MEDLINE=20079591; PubMed=10611322; DOI=10.1073/pnas.96.26.14973;  
 Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;  
 "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation  
 in response to DNA damage.";  
 Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).  
 [16]  
 RP  
 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 25-109 IN COMPLEX WITH P53.  
 MEDLINE=97081050; PubMed=8875929; DOI=10.1126/science.274.5289.948;  
 Kusie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,  
 Levine A.J., Pavletich N.P.;  
 "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor  
 transactivation domain.";  
 Science 274:948-953(1996).  
 [17]  
 CC  
 -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
 apoptosis by binding its transcriptional activation domain.  
 Functions as a ubiquitin ligase E3, in the presence of E1 and E2,

CC  
 toward p53 and itself. Permits the nuclear export of p53 and  
 targets it for proteasome-mediated proteolysis.  
 CC  
 -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.  
 CC  
 -!- SUBUNIT: Binds p53, p73, ARF(p14), ribosomal protein L5 and  
 specifically to RNA. Can interact also with retinoblastoma protein  
 (RB), E1A-associated protein p300 and the E2F1 transcription  
 factor.  
 CC  
 -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
 predominantly in the nucleoplasm. Interaction with ARF(p14)  
 results in the localization of both proteins to the nucleolus. The  
 nuclear localization signals in both ARF(p14) and MDM2 may be  
 necessary to allow efficient nucleolar localization of both  
 proteins.  
 CC  
 -!- ALTERNATIVE PRODUCTS:  
 CC  
 Event=Alternative splicing; Named isoforms=8;  
 CC  
 Name=Mdm2;  
 CC  
 IsoId=Q00987-1; Sequence=Displayed;  
 CC  
 Name=Mdm2-A;  
 CC  
 IsoId=Q00987-2; Sequence=VSP\_003208;  
 CC  
 Name=Mdm2-A1;  
 CC  
 IsoId=Q00987-3; Sequence=VSP\_003208, VSP\_003214;  
 CC  
 Name=Mdm2-B;  
 CC  
 IsoId=Q00987-4; Sequence=VSP\_003209;  
 CC  
 Name=Mdm2-C;  
 CC  
 IsoId=Q00987-5; Sequence=VSP\_003211;  
 CC  
 Name=Mdm2-D;  
 CC  
 IsoId=Q00987-6; Sequence=VSP\_003210;  
 CC  
 Name=Mdm2-E;  
 CC  
 IsoId=Q00987-7; Sequence=VSP\_003212, VSP\_003213;  
 CC  
 Name=Mdm2-alpha;  
 CC  
 IsoId=Q00987-8; Sequence=VSP\_003207;  
 CC  
 -!- TISSUE SPECIFICITY: Ubiquitous. Isoforms MDM2-A, -B, -C, -D and -E  
 are observed in a range of human cancers but absent in normal  
 tissues.  
 CC  
 -!- INDUCTION: By DNA damage.  
 CC  
 -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
 G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
 CC  
 Region II contains most of a central acidic region required for  
 interaction with ribosomal protein L5 and a putative C4-type zinc  
 finger. The RING finger domain which coordinates two molecules of  
 zinc interacts specifically with RNA whether or not zinc is  
 present and mediates the hetero-oligomerization with MDM4. It is  
 also essential for its ubiquitin ligase E3 activity toward p53 and  
 itself.  
 CC  
 -!- PTM: Phosphorylated in response to ionizing radiation in an ATM-  
 dependent manner.  
 CC  
 -!- DISEASE: Seems to be amplified in certain tumors (including soft  
 tissue sarcomas, osteosarcomas and gliomas). A higher frequency of  
 splice variants lacking p53 binding domain sequences was found in  
 late-stage and high-grade ovarian and bladder carcinomas. Four of  
 the splice variants show loss of p53 binding.  
 CC  
 -!- MISCELLANEOUS: MDM2 RING finger mutations that failed to  
 Query Match 98.9%; Score 548; DB 1; Length 491;  
 Best Local Similarity 99.1%; Pred. No. 2.4e-50;  
 Matches 108; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDYTMKEVLVFLGQYIMTKRLYDEKQOHVH 60  
 Db 17 SQIPASEQETLVVRPKPLLLKLLKSVGAQKDYTMKEVLVFLGQYIMTKRLYDEKQOHV 75  
 QY 61 CSNDLLGLDFGVPSFSVKEHKRYITMYIRNLVNVNQSSDSGTSVSEN 109  
 Db 77 CSNDLLGLDFGVPSFSVKEHKRYITMYIRNLVNVNQSSDSGTSVSEN 125  
 RESULT 5  
 MDM2 CANFA  
 ID MDM2 CANFA STANDARD; PRT; 487 AA.  
 AC P56950; Q95K05;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein  
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Cdm2).  
GN Name=Mdm2;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE OF 1-484 FROM N.A.  
RX MEDLINE=20219866; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;  
RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,  
RA Argyle D.J.;  
RT "Cloning, sequence analysis and expression of the cDNAs encoding the  
RT canine and equine homologues of the mouse double minute 2 (mdm2)  
RT proto-oncogene.";  
RL Cancer Lett. 152:9-13 (2000).  
[2]  
RP SEQUENCE FROM N.A. (ISOFORMS MDM2 AND MDM2-ALPHA).  
RX MEDLINE=20065171; PubMed=10597303; DOI=10.1038/sj.onc.1203182;  
RA Velthoen N., Metcalfe S., Milner J.;  
RT "A novel exon within the mdm2 gene modulates translation initiation in  
RT vitro and disrupts the p53-binding domain of mdm2 protein.";  
RL Oncogene 18:7026-7033 (1999).  
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and  
CC apoptosis by binding its transcriptional activation domain.  
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,  
CC toward p53 and itself. Permits the nuclear export of p53 and  
CC targets it for proteasome-mediated proteolysis (By similarity).  
CC -!- COPACITOR: Zinc is required for ubiquitin ligase E3 activity (By  
CC similarity).  
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and  
CC specifically to RNA. Can interact also with retinoblastoma protein  
CC (RB), E1A-associated protein EP300 and the E2F1 transcription  
CC factor (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed  
CC predominantly in the nucleoplasm (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Mdm2;  
CC IsoId=P56950-1; Sequence=Displayed;  
CC Name=Mdm2-alpha;  
CC IsoId=P56950-2; Sequence=VSP\_003206;  
CC -!- TISSUE SPECIFICITY: Isoform Mdm2-alpha is present in lymphoid and  
CC testicular tissues.  
CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its  
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.  
CC Region II contains most of a central acidic region required for  
CC interaction with ribosomal protein L5 and a putative C4-type zinc  
CC finger. The RING finger domain which coordinates two molecules of  
CC zinc interacts specifically with RNA whether or not zinc is  
CC present and mediates the hetero-oligomerization with MDM4. It is  
CC also essential for its ubiquitin ligase E3 activity toward p53 and  
CC itself (By similarity).  
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC -!- SIMILARITY: Contains 1 SWIB domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF100705; AAF67833.1; -;  
DR EMBL; AF322416; AAG42840.1; -;  
DR HSP; Q9UMT8; 1YCR.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_RanBP2\_1; 1.  
DR InterPro; IPR001841; Znf\_RanBP2\_2; 1.

DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS00199; ZF\_RANBP2\_2; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS00089; ZF\_RING\_2; 1.  
KW Alternative splicing; Ligase; Metal-binding; Nuclear protein;  
KW Ubiquitin conjugation pathway; Zinc; Zinc-finger.  
FT DOMAIN 27 107 SWIB  
FT DOMAIN 179 185 Nuclear localization signal (Potential).  
FT DOMAIN 190 202 Nuclear export signal.  
FT DOMAIN 210 304 ARP-binding.  
FT DOMAIN 210 215 Poly-Ser.  
FT DOMAIN 242 331 Region II.  
FT DOMAIN 243 301 Asp/Glu-rich (acidic).  
FT ZN\_FING 299 328 RanBP2-type.  
FT ZN\_FING 434 475 RING-type.  
FT DOMAIN 462 469 Nuclear localization signal  
(Potential).  
FT VARSPLIC 1 61 Missing (in isoform Mdm2-alpha).  
FT CONFLICT 11 11 /FTid=VSP\_003206.  
FT CONFLICT 238 239 G -> D (in Ref. 2).  
SQ SEQUENCE 487 AA; 54696 MW; 60CDB470A32A8E69 CRC64;  
Query Match 96.8%; Score 536; DB 1; Length 487;  
Best Local Similarity 96.3%; Pred. No. 4.7e-49;  
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 SQIPASEQETLVRPKPLLLKLLKSVGAQKQTYTMKEVLFYLGQYIMTKRLYDEKQHHVH 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQKQTYTMKEVLFYLGQYIMTKRLYDEKQHHV 76  
Qy 61 CSNDLLGDLFGVPSFVKHKKIYTMIRNLLVNVNQESSDSCTSVSEN 109  
Db 77 CSNDLLGDLFGVPSFVKHKKIYTMIRNLLVNVNQESSDSCTSVSEN 125  
RESULT 6  
Q9GMZ6 PRELIMINARY; PRT; 487 AA.  
AC Q9GMZ6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MDM2.  
GN Name=mdm2;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Setoguchi A., Tsujimoto H.;  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB031276; BAB11975.1; -;  
DR HSP; Q9UMT8; 1YCR.  
DR GO; GO:0005730; C:nucleolus; ISS.  
DR GO; GO:0005654; C:nucleoplasm; ISS.  
DR GO; GO:0017163; F:negative regulator of basal transcription a...; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0001022; P:negative regulation of transcription from P...; ISS.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB\_MDM2.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_RanBP2\_1.  
DR Pfam; PF00641; zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_2; 1.

```
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 487 AA; 54724 MW; 34FCSCG6A18D7744 CRC64;

Query Match
Best Local Similarity 96.8%; Score 536; DB 2; Length 487;
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRPKLLKLLKSVGAQKDYTTMKVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASQETLVPRPKLLKLLKSVGAQKDYTTMKVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFVSKHKRYITMYRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDFGVPSFVSKHKRYITMYRNLVVNNQHPDSGTSVSEN 125

RESULT 7
MDM2_HORSE STANDARD; PRT; 491 AA.
AC P56951;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Edm2).
GN Name=MDM2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20218666; PubMed=10754200; DOI=10.1016/S0304-3835(99)00427-9;
RA Nasir L., Burr P.D., McFarlane S.T., Gault E., Thompson H.,
RA Argyle D.J.;
RT Cloning, sequence analysis and expression of the cDNAs encoding the
RT canine and equine homologues of the mouse double minute 2 (mdm2)
RT proto-oncogene."
RL Cancer Lett. 152:9-13 (2000).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis (By similarity).
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity (By
CC similarity).
CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm (By similarity).
CC -!- DOMAIN: Region 1 is sufficient for binding p53 and inhibiting its
CC G1 arrest and apoptosis functions. It also binds p73 and E2F1.
CC Region II contains most of a central acidic region required for
CC interaction with ribosomal protein L5 and a putative C4-type zinc
CC finger. The RING finger domain which coordinates two molecules of
CC zinc interacts specifically with RNA whether or not zinc is
CC present and mediates the hetero-oligomerization with MDM4. It is
CC also essential for its ubiquitin ligase E3 activity toward p53 and
CC itself (By similarity).
CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.
CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 1 SWIB domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

```
CC EMBL; AF121140; AAF28866.1; -.
DR HSP; Q9UMT8; 1YCR.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB.
DR InterPro; IPR001876; Znf_RanBP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF0641; Zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS01199; ZF_RANBP2_2; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Ligase; Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW Zinc-finger.
FT DOMAIN 27 107 SWIB.
FT DOMAIN 179 185 Nuclear localization signal (Potential).
FT DOMAIN 190 202 Nuclear export signal.
FT DOMAIN 210 304 ARF-binding.
FT DOMAIN 210 215 Poly-Ser.
FT DOMAIN 242 331 Region II.
FT DOMAIN 243 301 Asp/Glu-rich (acidic).
FT ZN_FING 299 328 RanBP2-type.
FT ZN_FING 438 479 RING-type.
FT DOMAIN 466 473 Nucleolar localization signal
(Potential).
SQ SEQUENCE 491 AA; 55279 MW; 641E033D5C1DEC39 CRC64;

Query Match 96.8%; Score 536; DB 1; Length 491;
Best Local Similarity 96.3%; Pred. No. 4.8e-49;
Matches 105; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SQIPASQETLVPRPKLLKLLKSVGAQKDYTTMKVLFYLGQYIMTKRLYDEKQOHIVH 60
Db 17 SQIPASQETLVPRPKLLKLLKSVGAQKDYTTMKVLFYLGQYIMTKRLYDEKQOHIVY 76

Qy 61 CSNDLLGLDFGVPSFVSKHKRYITMYRNLVVNNQESSDSGTSVSEN 109
Db 77 CSNDLLGLDFGVPSFVSKHKRYITMYRNLVVNNQHPDSGTSVSEN 125

RESULT 8
QYRZ8
ID Q7YRZ8 PRELIMINARY; PRT; 491 AA.
AC Q7YRZ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Double minute 2 protein MDM2.
GN Name=mdm2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RA Miki R., Okuda M., Ma Z., Inokuma H., Onishi T.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB099709; BAC78209.1; -.
DR GO; GO:0005730; C:nucleolus; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0017163; F:negative regulator of basal transcription a.; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:000122; P:negative regulation of transcription from P.; ISS.
DR InterPro; IPR010984; MDM2.
DR InterPro; IPR003121; SWIB_MDM2.
DR InterPro; IPR001876; Znf_RanBP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF0641; Zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
```

```

DR PROSITE; PS50199; ZF_RANBP2_2; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 491 AA; 55433 MW; D93E25D638E88934 CRC64;

Query Match          96.2%; Score 533; DB 2; Length 491;
Best Local Similarity 95.4%; Pred. No. 1e-48; 2; Indels 0; Gaps 0;
Matches 104; Conservative 3; Mismatches 2;

QY 1 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVH 60
Db 17 SQMPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMVYRNLLVNVNQSSSGTSVSEN 109
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMVYRNLLVNVNQHEPSPSGTSVSEN 125

RESULT 9
Q8WYJ2 ID Q8WYJ2 PRELIMINARY; PRT; 436 AA.
AC Q8WYJ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MDM2 protein.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90);
RX MEDLINE=21248713; PubMed=11351297;
RA Tamborini E., Della Torre G., Lavarino C., Azzarelli A.,
RA Carpinelli P., Pierotti M.A., Pilotti S.;
RT "Analysis of the molecular species generated by MDM2 gene
RT amplification in liposarcomas.";
RL Int. J. Cancer 92:790-796(2001).
DR EMBL; AF092844; AAL40179.1; -.
DR HSP; Q9UNT8; 1YCR.
DR GO; GO:0005730; C:nucleolus; ISS.
DR GO; GO:0005654; C:nucleoplasm; ISS.
DR GO; GO:0007163; F:negative regulator of basal transcription a. . .; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0000122; P:negative regulation of transcription from P. . .; ISS.
DR Pfam; PF02201; SWIB; 1.
DR Pfam; PF00641; zf-RanBP; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01358; ZF_RANBP2_1; 1.
DR PROSITE; PS50199; ZF_RANBP2_2; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 436 AA; 49248 MW; 3C9F55E98BC4203A CRC64;

Query Match          89.9%; Score 498; DB 2; Length 436;
Best Local Similarity 93.3%; Pred. No. 5.2e-45;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVH 60
Db 17 SQIPASEQETLVRPKLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQKHIVY 76

QY 61 CSNDLLGDLFGVPSFSVKEHRKIYTMVYRNLLVNVNQSSSGTS 105
Db 77 CSNDLLGDLFGVPSFSVKEHRKIYTMVYRNLLVNVNQHEPSPSGTS 121

RESULT 10
MDM2_MOUSE ID MDM2_MOUSE STANDARD; PRT; 489 AA.
AC P23804; Q61040; Q64330;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

```

DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein
DE Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein).
GN Name=Mdm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX MEDLINE=91224107; PubMed=2026149;
RA Fatharzadeh S.S., Trusko S.P., George D.L.;
RT "Tumorigenic potential associated with enhanced expression of a gene
RT that is amplified in a mouse tumor cell line.";
RL EMBO J. 10:1565-1569(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX STRAIN=129/SV;
RX MEDLINE=97074674; PubMed=8917101; DOI=10.1016/0378-1119(96)00151-5;
RA Jones S.N., Ansari-Lari M.A., Hancock A.R., Jones W.J., Gibbs R.A.,
RA Donehower L.A., Bradley A.;
RT "Genomic organization of the mouse double minute 2 gene.";
RL Gene 175:209-213(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM MDM2-P90).
RX STRAIN=129/SV;
RX MEDLINE=96299630; PubMed=8660994; DOI=10.1006/geno.1996.0210;
RA de Oca Luna R.M., Tabor A.D., Eberspaecher H., Hulboy D.L.,
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "Multiple murine double minute gene 2 (MDM2) proteins are induced by
RT ultraviolet light.";
RL J. Biol. Chem. 274:8161-8168(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=99175199; PubMed=10075719; DOI=10.1074/jbc.274.12.8161;
RA Saucedo L.J., Myers C.D., Perry M.E.;
RT "The organization and expression of the mdm2 gene.";
RL Genomics 33:352-357(1996).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS MDM2-P90 AND MDM2-P76).
RX MEDLINE=20180080; PubMed=10713175;
RX DOI=10.1128/MCB.20.7.2517-2528.2000;
RA Weber J.D., Kuo M.-L., Bothner B., DiGiannarino E.L., Kriwacki R.W.,
RA Rousset M.F., Sherr C.J.;
RT "Cooperative signals governing ARF-mdm2 interaction and nucleolar
RT localization of the complex.";
RL Mol. Cell. Biol. 20:2517-2528(2000).
RN [6]
RP PHOSPHORYLATION BY ATM.
RX MEDLINE=20079591; PubMed=10611322; DOI=10.1073/pnas.96.26.14973;
RA Khosravi R., Maya R., Gottlieb T., Oren M., Shiloh Y., Shkedy D.;
RT "Rapid ATM-dependent phosphorylation of MDM2 precedes p53 accumulation
RT in response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14973-14977(1999).
CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and
CC apoptosis by binding its transcriptional activation domain.
CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2,
CC toward p53 and itself. Permits the nuclear export of p53 and
CC targets it for proteasome-mediated proteolysis.
CC -!- COFACTOR: Zinc is required for ubiquitin ligase E3 activity.
CC -!- SUBUNIT: Binds p53, p73, ARF(P14), ribosomal protein L5 and
CC specifically to RNA. Can interact also with retinoblastoma protein
CC (RB), E1A-associated protein EP300 and the E2F1 transcription
CC factor.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed
CC predominantly in the nucleoplasm. Interaction with ARF(P14)
CC results in the localization of both proteins to the nucleolus. The
CC nucleolar localization signals in both ARF(P14) and MDM2 may be
CC necessary to allow efficient nucleolar localization of both
CC proteins.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Mdm2-p90;
CC IsoId=P23804-1; Sequence=Displayed;

```

Note-Isoform Mdm2-p76 can also be produced by alternative initiation at Met-50 of isoform Mdm2-p90, but is produced more efficiently by alternative splicing;  
Name=Mdm2-p76;  
IsoId=P23804-2; Sequence=VSP\_003215;  
Note=Does not bind to p53;  
Event=Alternative initiation;  
Comment=2 isoforms, Mdm2-p90 (shown here) and Mdm2-p76, are produced by alternative initiation at Met-1 and Met-50. Isoform Mdm2-p76 is produced more efficiently by alternative splicing;  
-!- TISSUE SPECIFICITY: Ubiquitously expressed at low-level throughout embryo development and in adult tissues. Mdm2-p90 is much more abundant than Mdm2-p76 in testis, brain, heart, and kidney, but in the thymus, spleen, and intestine, the levels of the MDM2 proteins are roughly equivalent.  
-!- INDUCTION: By UV light.  
-!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself.  
-!- PTM: Phosphorylated in response to ionizing radiation in an ATM-dependent manner.  
-!- DISEASE: The gene for this protein is amplified in a mouse tumor cell line.  
-!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
-!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
-!- SIMILARITY: Contains 1 RING-type zinc finger.  
-!- SIMILARITY: Contains 1 SWIB domain.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; X58876; CAA41684.1; -;  
DR EMBL; U40145; AAA91167.1; -;  
DR EMBL; U47944; AAB09030.1; -;  
DR EMBL; U47935; AAB09030.1; JOINED.  
DR EMBL; U47936; AAB09030.1; JOINED.  
DR EMBL; U47937; AAB09030.1; JOINED.  
DR EMBL; U47938; AAB09030.1; JOINED.  
DR EMBL; U47939; AAB09030.1; JOINED.  
DR EMBL; U47940; AAB09030.1; JOINED.  
DR EMBL; U47941; AAB09030.1; JOINED.  
DR EMBL; U47942; AAB09030.1; JOINED.  
DR EMBL; U47943; AAB09030.1; JOINED.  
DR EMBL; U47934; AAB09031.1; -;  
DR PIR; S15349; S15349.  
DR HSSP; Q9UMT8; 1YCR.  
DR MGD; MGI:96952; Mdm2.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IDA.  
DR GO; GO:0030163; P:protein catabolism; IDA.  
DR GO; GO:0016567; P:protein ubiquitination; IDA.  
DR GO; GO:0007089; P:traversing start control point of mitotic c. .; IDA.  
DR InterPro; IPR010984; MDM2.  
DR InterPro; IPR003121; SWIB.  
DR InterPro; IPR001876; Znf\_RanGDP.  
DR InterPro; IPR001841; Znf\_Ring.  
DR Pfam; PF02201; SWIB; 1.  
DR Pfam; PF00641; zf-RanBP; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
DR PROSITE; PS01199; ZF\_RANBP2\_2; 1.

DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
DR PROSITE; PS0089; ZF\_RING\_2; 1.  
KW Alternative initiation; Alternation; Ligase; Metal-binding;  
KW Nuclear protein; Phosphorylation; Proto-oncogene;  
KW Ub1 conjugation pathway; Zinc; Zinc-finger.  
FT CHAIN 1 489 Ubiquitin-protein ligase E3 Mdm2, isoform Mdm2-p90.  
FT CHAIN 50 489 Ubiquitin-protein ligase E3 Mdm2, isoform Mdm2-p76.  
FT INIT MET 50 50 For isoform Mdm2-p76.  
FT DOMAIN 27 107 SWIB.  
FT DOMAIN 176 182 Nuclear localization signal (Potential).  
FT DOMAIN 183 195 Nuclear export signal.  
FT DOMAIN 203 213 Poly-Ser.  
FT DOMAIN 208 302 ARP-binding.  
FT DOMAIN 221 329 Region II.  
FT DOMAIN 221 299 Asp/Glu-rich (acidic).  
FT ZN\_FING 297 326 RanBP2-type.  
FT ZN\_FING 436 477 RING-type.  
FT DOMAIN 464 471 Nucleolar localization signal (Potential).  
FT VARSPPLIC 1 49 Missing (in isoform Mdm2-p76).  
FT CONFLICT 203 203 S -> T (in Ref. 1).  
FT CONFLICT 419 419 D -> H (in Ref. 1).  
FT CONFLICT 486 486 S -> T (in Ref. 3).  
SQ SEQUENCE 489 AA; 54543 MW; 4ABF489E92038DF4 CRC64;  
Query Match 88.2%; Score 488.5; DB 1; Length 489;  
Best Local Similarity 87.2%; Pred. No. 6.2e-44;  
Matches 95; Conservative 8; Mismatches 3; Indels 3; Gaps 1;  
QY 1 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTKWKEIFYIGQYIMTKRLYDEKQOHIV 60  
Db 17 SQIPASEQETLVRPKPLLLKLLKSVGAQNDYTKWKEIFYIGQYIMTKRLYDEKQOHIV 76  
QY 61 CSNDLLGDLGVPSFVSKHRKIYTMVYRNVLVNVNQSSDSCTSVSEN 109  
Db 77 CSNDLLGDLGVPSFVSKHRKIYTMVYRNVLVNVNQSSDSCTSVSEN 122  
RESULT 11  
Q91XK7 PRELIMINARY; PRT; 489 AA.  
AC Q91XK7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200011P22 product:transformed mouse 3T3 cell double minute 2, full insert sequence (transformed mouse 3T3 cell double minute 2, musculus 2 days neonate thymic cells cDNA, RIKEN full-length enriched library, clone:E43002B10 product:transformed mouse 3T3 cell double minute 2, full insert sequence).  
GN Name=Mdm2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;  
RX MEDLINE=95279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J, and NOD; TISSUE=lung, and Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).





DR Pfam; PF02201; SWIB; 1.  
 FT NON\_TER 118 118  
 SQ SEQUENCE 118 AA; 13536 MW; D7A4DBAA83D8841B CRC64;

Query Match 85.0%; Score 471; DB 2; Length 118;  
 Best Local Similarity 98.9%; Pred. No. 9.4e-43;  
 Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60  
 DB 17 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVY 76

QY 61 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNLV 93  
 DB 77 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNLV 109

RESULT 13  
 MDM2\_MESAU STANDARD; PRT; 466 AA.  
 ID MDM2\_MESAU  
 AC Q60524;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ubiquitin-protein ligase E3 Mdm2 (EC 6.3.2.-) (p53-binding protein Mdm2) (Oncoprotein Mdm2) (Double minute 2 protein) (Fragment).  
 GN Name=MDM2;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=95300112; PubMed=7780969;  
 RA Chang K.W., Leoni S., Mangold K.A., Hübchak S., Scarpelli D.G.;  
 RT "Multiple genetic alterations in hamster pancreatic ductal adenocarcinomas";  
 RL Cancer Res. 55:2560-2568 (1995).  
 CC -!- FUNCTION: Inhibits p53- and p73-mediated cell cycle arrest and apoptosis by binding its transcriptional activation domain.  
 CC Functions as a ubiquitin ligase E3, in the presence of E1 and E2, toward p53 and itself. Permits the nuclear export of p53 and targets it for proteasome-mediated proteolysis (By similarity).  
 CC -!- COPACITOR: Zinc is required for ubiquitin ligase E3 activity (By similarity).  
 CC -!- SUBUNIT: Binds p53, p73, ARF (P14), ribosomal protein L5 and specifically to RNA. Can interact also with retinoblastoma protein (RB), E1A-associated protein BP300 and the E2F1 transcription factor (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Expressed predominantly in the nucleoplasm (By similarity).  
 CC -!- DOMAIN: Region I is sufficient for binding p53 and inhibiting its G1 arrest and apoptosis functions. It also binds p73 and E2F1. Region II contains most of a central acidic region required for interaction with ribosomal protein L5 and a putative C4-type zinc finger. The RING finger domain which coordinates two molecules of zinc interacts specifically with RNA whether or not zinc is present and mediates the hetero-oligomerization with MDM4. It is also essential for its ubiquitin ligase E3 activity toward p53 and itself (By similarity).  
 CC -!- DISEASE: The gene for this protein is overexpressed in some tumors.  
 CC -!- SIMILARITY: Belongs to the MDM2 / MDM4 family.  
 CC -!- SIMILARITY: Contains 1 RanBP2-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.  
 CC -!- SIMILARITY: Contains 1 SWIB domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U10982; AAC52425.1; -.  
 DR HSSP; Q9UMT8; LYCR.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB.  
 DR InterPro; IPR001876; Znf\_RangDP.  
 DR InterPro; IPR001841; Znf\_Ring.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.  
 DR PROSITE; PS01359; ZF\_RANBP2\_2; 1.  
 DR PROSITE; PS05018; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE; PS05089; ZF\_RING\_2; 1.  
 KW Ligase; Metal-binding; Nuclear protein; Proto-oncogene;  
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.  
 FT NON\_TER 1  
 FT DOMAIN 1 98 SWIB.  
 FT DOMAIN 169 175 Nuclear localization signal (Potential).  
 FT DOMAIN 176 188 Nuclear export signal.  
 FT DOMAIN 196 201 Poly-Ser.  
 FT DOMAIN 196 290 ARF-binding.  
 FT DOMAIN 228 317 Region II.  
 FT DOMAIN 209 314 Asp/Glu-rich (acidic).  
 FT ZN\_FING 285 314 RanBP2-type.  
 FT ZN\_FING 419 460 RING-type.  
 FT DOMAIN 447 454 Nucleolar localization signal (Potential).  
 FT NON\_TER 466  
 FT SEQUENCE 466 AA; 52390 MW; 78A3042163C5F939 CRC64;  
 SQ SEQUENCE 466 AA; 52390 MW; 78A3042163C5F939 CRC64;

Query Match 83.8%; Score 464.5; DB 1; Length 466;  
 Best Local Similarity 85.3%; Pred. No. 2.3e-41;  
 Matches 93; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

QY 1 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVH 60  
 DB 9 SQIPASEQETLVPRPKLLKLLKSVGAQKDYTMKEVLYFGQYIMTKRLYDEKQOHIVY 67

QY 61 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNLV 109  
 DB 68 CSNDLLGLDGLFGVPSFVKHEHRIYTMIRNLV 116

RESULT 14  
 Q9PVL2 PRELIMINARY; PRT; 325 AA.  
 ID Q9PVL2  
 AC Q9PVL2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE MDM2 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA LaFleur D.A., Foster D.N.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF005045; AAF04192.1; -.  
 DR HSSP; Q9UMT8; LYCR.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR InterPro; IPR010984; MDM2.  
 DR InterPro; IPR003121; SWIB.  
 DR Pfam; PF02201; SWIB; 1.  
 DR Pfam; PF00641; zf-RanBP; 1.  
 DR PROSITE; PS01358; ZF\_RANBP2\_1; 1.

Search completed: February 16, 2005, 08:24:05  
Job time : 172 secs